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Sequence 4, Appl1 Sequence 2, Appl1 Sequence 16, Appl Sequence 166, App Sequence 166, App Sequence 3, Appl1 Sequence 5, Appl1 Sequence 5, Appl1 Sequence 7, Appl1 Sequence 2, Appl1
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Pred. No. 3.8;
1; Mismatches 1; Indels
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM PC. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/822,966B
FILING DATE: January 17, 1992
ATTORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 06530/052001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1872-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Steven J. Burakoff
APPLICANT: Steven J. Burakoff
APPLICANT: Steven J. Burakoff
APPLICANT: Steven J. Burbar
APPLICANT: Steven J. Burbar
TITLE OF INVENTION: IMMUNOPHILIN
NUMBER OF ESQUENCES: 6
CORRESSED ADDRESS:
ADDRESSED: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITT: Boston
STATE: Massachusetts
US-09-359-257-4
US-08-835-170-2
US-09-259-257-2
US-08-484-631-166
US-08-487-570-166
US-08-827-570-166
US-08-609-443B-3
US-08-609-443B-3
US-08-609-443B-7
US-08-609-443B-7
US-08-609-443B-7
US-08-609-443B-7
US-08-609-063C-7
US-08-609-063C-7
US-08-609-063C-7
US-08-609-063C-7
US-08-609-063C-7
US-08-609-063C-7
US-08-569-063C-7
US-08-569-063C-7
US-08-569-063C-7
US-08-569-063C-7
US-08-569-063C-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07822966B Patent No. 5498597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02110-2804
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KKRVDHC 20
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US-07-822-966B-4
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292.168 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-822-9668-6
US-08-803-899-6
US-08-803-899-6
US-09-006-783A-7
US-09-258-371-10
US-09-499-082-10
US-09-499-082-10
US-09-659-166-2
US-09-659-166-2
US-09-659-166-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-822-966B-4
US-08-336-618-19
PCT-US92-03993-5
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5.08-892-770-5
5.09-231-529-6
5.08-977-816-6
5.09-039-859-9
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                               US-09-606-129A-18
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Match Length
                                                                                                                                                                                                                                                                                                                                                                       1 KKRIMHC 7
                                                                                                                                                                                                     November
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                                                                                                                                                                                                     Run on:
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Gaps

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78.0%; Score 32; DB 5; Length 99; 71.4%; Pred. No. 9.1;
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                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/07822966B
Patent No. 5498597
GENERAL INFORMATION:
APPLICANT: Steven J. Burakoff
APPLICANT: Stuart L. Schreiber
APPLICANT: Barbara E. Blerer
TITLE OF INVENTION: IEMPLOALIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 50.2 or 55sx
COMPUTER: 18M PS/2 Model 50.0 SOFTWARE: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
APPLICATION DATA:
APPLICATION NUMBER: US/07/822,966B
FILING DATE: January 17, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REBERENGE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/052001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) $42-5070
                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-WAY-1991
ATTORNEY/AGENT INFORMATION:
                                   COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4 Matches 5; Conservative
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ZIP: 02110-2804
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TELEX: 200154
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US92-03993-5
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                             Sequence 19, Application US/08336618
Fatent No. 5763590
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: DRAFT
TITLE OF INVENTION: DRAFT
TITLE OF INVENTION: DRAFT
TITLE OF SEQUENCES:
AUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: Two Militia Drive
STREET: Wassachusetts
CONNEY. U.S.A.
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TITLE OF INVENTION: REKEP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN NUMBER OF ENDENCES: 10

CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB ]
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION 1973

APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-0CT-1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
RESISTRATION NUMBER: VP191-06A
RESISTRATION NUMBER: VP191-06A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPI91-06A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application PC/TUS9203993 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540
INFOMATION FOR SEQ ID NO: 19:
SEGUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-336-618-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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14 KKRVDHC 20
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                 US-08-336-618-19
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PCT-US92-03993-5
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Gaps

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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WANG, TONGWEN
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR ENHANCING
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR ENHANCING
TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASTINGTON
STATE: DC
                                                                                                                                                                             Score 32; DB 1; Length 141;
Pred. No. 13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N 78.0%; Score 32; DB 2; Length 141; Similarity 71.4%; Pred. No. 13; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,899
FILING DATE: 02/21/1997
CLASSIFICATION ST4
PRIOR APPLICATION NUMBER: 60/012,054
FILING DATE: 02/22/196
CLASSIFICATION NUMBER: 60/012,054
FILING DATE: 02/22/196
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0609.4240001
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NAME: STEFFE, ERIC K.
REGISTRATION UNDBER: 36,688
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)371-2540
INFORMATION FOR SEO ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   US-08-803-899-6; Sequence 6, Application US/08803899; Patent No. 5912224
                                 LENGTH: 141 amino acids
TYPE: amino acid
STRANDENNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-822-9668-6
                                                                                                                                                                             78.0%;
ilarity 71.4%;
Conservative
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INFORMATION FOR SEQ ID NO:
                SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
Matches 5; Conserva
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                      111: 11
35 KKRVDHC 41
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TOPOLOGY: 1
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NEASOLL V.
195-08-336-618-18
Sequence 18, Application US/08336618
Sequence 18, Application US/08336618
Sequence 18, Application US/08336618
Sequence 18, Application US/08336618
Sequence 18, Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND
TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/7/77,752
APPLICATION NUMBER: US/7/77,752
APPLICATION NUMBER: US/7/77,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION NUMBER: PCT/
FILING DATE: 11-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: YPI91-06A
TELEPHONE: G17-861-6540
INFORMATION FOR SEO ID NO: 18:
INFORMATION FOR SEO ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h
Similarity 71.4%; Pred. No. 13:
5; Conservative 1; Mismatchee 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-336-618-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity
Matches 5; Conserv
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36 KKRVDHC 42
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Gaps
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                                                                                                                                 DB 4; Length 269;
24;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.0%; Score 32; DB 2; 57.1%; Pred. No. 26; tive 3; Mismatches
                                                                                                                                                                           3; Mismatches
                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       028722-144
                                                                                                                                                                                                                                                                                                                            US-09-258-371-10
; Sequence 10, Application US/09258371
; Petent No. 5986078
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-751-230-10
; Sequence 10, Application US/08751230
; Patent No. 6117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/POCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-4400
TELEFAX: 415-854-8275
                                                                                                                                   78.0%;
57.1%;
                  I: 269 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 294 amino acids TYPE: amino acid
                                                                                                                                   Query Match 78.0
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-006-783A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein US-09-258-371-10
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Best Local Similarity
The 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                      |:|::||
67 KRRMLHC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 KRRMLHC 88
                                                                                                                                                                                                             1 KKRIMHC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKRIMHC 7
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Patent No. 6297366
GENERAL INFORMATION:
APPLICANT: Gudkavy VAPPLICANT: Gravestev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 5; Length.142;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MCDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: USA
21P: 60606
                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
                                                                                                                                                                                                     PROGRAPHICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEFANA: (617) 861-6240
INFORMATION FOR SEQ. ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY, AGENT INFORMATION:
NAME: NO. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 142 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein PCT-US92-03993-7
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                   FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111: 11
36 KKRVDHC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKRIMHC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-006-783A-5
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Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTONNEY, AGGNT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENTITLE OF INVENTION: SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNUBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 78.0%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            650-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-499-082-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alexandria
                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-09-258-372-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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APPLICANT: Garkattsev, Igor
APPLICANT: Riabowol, Rarl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Helbing, Caren C.
APPLICANT: Halbing, Karl
APPLICANT: Rabowol, Karl
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                          COUNTRY: USA
Z1D: 2213-1404
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILLNG DATE: 15-NOV-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
FILING DATE: 08-DEC-1995
ATTORNEY-AGENT INFORMATION:
NAME: MOOJ, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-14.
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09499082 Patent No. 6143522
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-751-230-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
GY: linear
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82 KRRMLHC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKRIMHC 7
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US-09-499-082-10
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Gaps

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FILE REFERENCE: GP-30218
CURRENT APPLICATION NUMBER: US/09/659,166
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: UK 9921505.5
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GH50002
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08802466; Patent No. 5972606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative 1
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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LENGTH: 528 amino acids
                                                                                                                                                                                                                                                       Query Match 78.0
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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267 KNRIIHC 273
                                                                                                                                                                                                  ; ORGANISM: rattus
US-09-659-166-2
                                                                                                                                                                                                                                                                                                                               1 KKRIMHC 7
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                                                                                                                                           SEQ ID NO 2
LENGTH: 527
TYPE: PRT
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US-08-802-466-2
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APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
TITLE OF INVENTION: Pathway
                                                                                                       DB 4; Length 294; 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 294;
26;
                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff STRET: 300 South Wacker Drive CITY: Chicago STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/006,783A
                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%; Score 32;
57.1%; Pred. No. 2
                                                                                                         Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/CAGENT INFORMATION:
NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97,837
                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09659166
; Patent No. 6355465
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , APPLICANT: CREASY, CARETHA LEE ... APPLICANT: TESTA, TANIA TAMSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                       78.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 294 amino acids
amino acid
                                                                                                         Query Match 78.0%
Best Local Similarity 57.1%
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.1
Matches 4; Conservative
LENGTH: 294 amino acids
                                TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-258-372-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                    amino acid
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82 KRRMLHC 88
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82 KRRMLHC 88
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                                                                                                                                                                                                                                                                        RESULT 13
US-09-006-783A-3
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US-09-659-166-2
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Length 527;
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                                 1; Indels
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                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Creasy, et al.
TITLE OF INVENTION: HUMAN PROFEIN KINASE HOACF72
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION OF SERVING SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,466
FILING DATE: 19 February 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
DB 4;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2;
Pred. No. 46;
1; Mismatches
                                 1; Mismatches
78.0%; Score 32;
71.4%; Pred. No. 4
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Db 268 KNRIIHC 274

Search completed: November 1, 2002, 14:51:57 Job time: 2.58521 secs

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Bovine mammary tis Human FKBP-13 immu

Human colon cancer Novel human secret

Amino acid sequenc

Amino acid sequenc Human P37ING1. Ho Tumour suppressor Amino acid sequenc Tumour suppressor Human p33ING1 poly Amino acid sequenc E. coli growth and Drosophila melanog Human protein kina Human protein kina Human protein kina Human acid sequenc Acidic leucine ami Acidic leucine ami Acidic leucine ami Novel human acid Novel human diagno Human immune/haema Novel human diagno Human immune/haema Novel human diagno Human immune/haema Novel human diagno Human immune/haema

Human transcriptio Drosophila melanog Bovine P58 protein

Novel human diagno

Cercospora nicotia Cercospora nicotia Human polypeptide,

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 34031.
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                                                                                                                                               AAE02011
AAY68781
AAW96316
AAW96315
ABG24213
AAU29777
ABG09069
                                                                                                                                                                                                                                              ABB62446
AAW36140
ABG09790
AAW71468
AAY99884
AAM93837
                                                                                                                                                                                                            AAM87522
ABG08440
                                                                                                                                                                                                                             ABB57919
ABB50167
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AAW64559
                                                                     AAE06676
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9905-0126785.
9905-0127462.
9905-012834.
9905-0138714.
9905-0130077.
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99US-0123180.
99US-0123548.
99US-0125788.
2000EP-0301439
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Arabidopsis thaliana.
25-FEB-2000;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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AAG28710;
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AAG28710
Murine INGb1 isofo
Murine P37ING1 pol
Arabidopsis thalia
Arabidopsis thalia
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Bovine FKBP-13 imm
Novel human diagno
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                                                         November 1, 2002, 14:40:53 ; Search time 1.58682 Seconds (without alignments) 489.985 Million cell updates/sec
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2. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                         747574 segs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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AAG48144
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ABG14241
AAG76114
AAY97245
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AAY97242
                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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82.9
82.9
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80.5
778.0
778.0
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01-APR-1999; 06-APR-1999; 08-APR-1999; 16-APR-1999; 19-APR-1999;

Human colon cancer Human INGbl isofor Bovine RFKBP, Bos

Score

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ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and enceres and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 gene, each having that own promoter have been discovered. Expression of one promoter (1a) produces a protein identical to ING1. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 can identical C-terminal fragment to ING1 but an additional 104 characteristics of an oncogene. When overexpressed in cells (even designated p371NG1 (Wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an included acid encoding exon 1b of ing1 by hybridisation with an included acid encoding exon 1b of ing1 by hybridisation with an included acid encoding exon 1b of ing1 by hybridisation with an include acid encoding exon 1b of ing1 by an order of exon 1b of ing1 by and ing1 by and ing1 by an order of exon 1b of ing1 by and ing1 by an order of exon 1b of ing1 by and ing1 by ing1 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
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Pred. No. 18;
3; Mismatches 0; Indels
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ilarity 57.1%;
Conservative 3
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Matches 4; Conserv
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67 KRRVLHC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; INC1; ing1; p33INC1; p37ING1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
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                          990S-0159638.
990S-0159584.
990S-0160741.
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990S-0161360.
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99US-0160981.
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99US-0161405.
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71.4%;
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5; Conserva
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06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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14 - MAY - 1999;
18 - MAY - 1999;
19 - MAY - 1999;
20 - MAY - 1999;
Nutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of the p53 gene many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1 encoded a tumour suppressor protein that functional within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative a produces a protein having each having their own promoter have been discovered. Expression of one promoter (1a) produces a protein has been destinated p37ING1 (wild type: p33ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 is able to cause of cancer and an oncogene. When overexpressed in cells cause concogenic form of ing1. Novel peptide sequences taken from the 104 Neterminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cells producers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 51;
3; Mismatches
                                       Disclosure; Fig 12; 134pp; English.
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99US-0125788.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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67 KRRVLHC 73
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99US-0155659.
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99US-0157753.
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 16 - JUL - 1999;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0158232.
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99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128234.

25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999;

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Pred. No. 1.5e+02;
3; Mismatches 0
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99US-0123180.
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99US-0128134.
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99US-0130891.
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99US-0159634.
99US-0159584.
99US-0160741.
99US-0160770.
99US-0160815.
99US-0160980.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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261 KRRLLHC 267
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24-SEP-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potentially smaller and therefore easier to introduce into cells than intact FKBP-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified mammalian FKBP-13 polypeptide capable of binding FK506 useful for identifying and studying immunosuppressant drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                     FKBP-13; immunophilin; FK506; rapamycin; rheumatoid arthritis; diabetes; organ transplant; graft versus host disease;
                                                                                                                                                                                                 Length 564;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                           AAR93552 standard; Peptide; 40 AA.
          990S-0160814.
99US-0160815.
99US-0160818.
99US-0160981.
99US-0161404.
99US-0161404.
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57.1%;
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292 KRRLLHC 298
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21-0CT-1999,
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03-NOV-1999;
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                  ;
                   DB 17; Length 40;
                   Score 32; DB 1
Pred. No. 20;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 44600; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #14232.
                                                                                                                                                                                                                                                                       ABG14241 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                78.0%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
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2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; AAS78428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                     14 KKRVDHC 20
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                                                                                                         1 KKRIMHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blodiversity
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                                                                                                                                                                                                                                                                                                                    ABG14241;
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                                                           Matches
                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                    ABG14241
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\$\text{2} \text{2} \t

78.0%; Score 32; DB 22; Length 83;

Query Match

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cancer associated nucleic actions (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
charapy and treatment of diseases associated with inappropriate P
cc expression. For example, N and P may be used to treat disorders
cassociated with decreased expression by rectifying mutations or deletions
cn in a patient's genome that affect the activity of P by expressing
cn inactive proteins or to supplement the patients own production of P.
Additionally, N may be used to produce the colon cancer-associated Ps,
cby inserting the nucleic acids into a host cell and culturing the cell
co express the proteins. N and P can be used in the prevention, diagnosis
cand treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
and AAB37789 represent sequences used in the exemplification of the
cross of time of publication, meaning no sequences listing were
missing at time of publication, meaning no sequences are present for
coverpressing at time of publication, meaning no sequences are present for
coverpressing at time of publication, meaning no sequences are present for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277~\mathrm{human} colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                    Human colon cancer antigen protein SEQ ID NO:6878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 8320-8322; 9803pp; English.
AAG76114 standard; Protein; 83 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000; 2000WO-US26524
                                                                                                                                                              03-SEP-2001 (first entry)
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Matches 5; Conserv
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48 KKRVDHC 54
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Nutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of the p53 gene many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with cremains unknown but p53 has been found to act in cooperation with corrected a tumour suppressor protein that functionad within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not within a region, that in ING1 mor significant variations in its cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer etiology. However, alternative initiation exons of the ing1 cancer expression of a second promoter (lb) produces a protein having the newly discovered protein having concept of an oncogene. When overexpressed in cells (even those expression of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NG1 has the coalse proliferation or transformation of ting1 by hybridisation with an concept of an oncogenic form of ing1. Novel peptide sequences taken from the 104 or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 or its antisense sequence can identify individuals expressing and expudence as identified and become indentify individuals expressing the study of the cancer of the cancer of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                     p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudkov A, Zeremski M, Gurova KV, Grigorian IA;
                                                                                                                                                                                                                                                                                                                          Human INGb1 isoform N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Figure 7a; 134pp; English.
                                                                               AAY97245 standard; Protein; 94 AA
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                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                               19-DEC-2000
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                                                                                                                                                               AAY97245;
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RESULT 10
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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                          Rapamycin; FK506; binding protein; RFKBP; prolyl isomerase; immunosupressant; cyclosporin A; macrolide; bovine; thymus; bRFKBP; cis-trans prolyl isomerase activity; FKBP12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prolyl isomerase and rapamycin FK506 binding protein - useful
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Score 32; DB 21; Length 94;
Pred. No. 45;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening potential immunosuppressive cpds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG03758 standard; Protein; 104 AA.
                                                                                                                                                             AAR28979 standard; protein; 99 AA.
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71.4%;
  78.0%;
57.1%;
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                                                                                                                                                                                                                    (first entry)
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VERT-) VERTEX PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.4 nes 5; Conservative
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              Best Local Similarity
Matches 4; Conserv
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67_KRRMLHC 73
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                                                        1 KKRIMHC 7
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                                                                                                                                                                                                                                               Bovine RFKBP
                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1991;
                                                                                                                                                                                                                    24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                 WO9219745-A.
                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harding MW;
                                                                                                                                                                                                                                                                                                                                      Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                        AAR28979;
    Query Match
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                                                                                                                                  RESULT 11
AAR28979
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This is the amino acid sequence of the human p28·ING1 protein, used in the method of the invention, involving the human p33·ING1 brotein. The ING1 gene encodes p33·ING1 which can be used to protein. The ING1 gene encodes p33·ING1 which can be used to modulate the activity of, isolate or detect p53. Expression of the control and p53 genes in a mammalian cell results in normal growth crequiation anchorage-dependent growth and apoptosis as a response to irreversible DNA damage and other cellular insult. Inhibition of expression of either gene results in a loss of cellular growth control, anchorage independent growth, inhibition of apoptosis and resistance to radiation and oytcoxic drugs. The p33·ING1 is a component of the p53 signalling pathway that cooperates with p53 in negative regulation of cell proliferation by modulating p53 dependent transcriptional activation. Biological function of p53 signalling pathway can therefore be regulated (both enhanced or suppressed) by modulating p33·ING1 activity. The modulation of p33·ING1 activity can be used for the stimulation or restoration of the p53 pathway in cantic cancer therapy or for the suppression of the p53 pathway to defend sensitive tissues from genotoxic stress or for the generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 20; Length 128;
Pred. No. 60;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine; mammary gland; cancer; tumour; anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine mammary tissue derived protein #47.
    /note- "p26-ING1 fragment"
                                                                                                                                                                                                                                                    (UNII ) UNIV ILLINOIS BOARD OF TRUSTEES. (UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                         Garkavtsev I, Gudkov A, Riabowol K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Page 61; 64pp; English.
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ilarity 57.1%;
Conservative
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                                                                                                                                        98WO-US18179
                                                                                                                                                                                   98US-0006783.
                                                                                                                                                                                                                                                                                                                                                                                                                Use of p33-ING1 peptides
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-263685/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 128 AA;
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                                                 WO9916790-A1
                                                                                                                                                                                   14-JAN-1998;
26-SEP-1997;
                                                                                                                                        24-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB87656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; p33-ING1 protein; growth regulation; apoptosis; DNA damage; inhibition; anchorage independent growth; cytotoxic drug; cancer; transcriptional activation; immortal cell line; p28-ING1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%; Score 32; DB 21; Length 104; 71.4%; Pred. No. 50; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the human p28-ING1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID 7839; 71pp + CD-ROM; English
                                               Human secreted protein, SEQ ID NO: 7839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers Misc_Difference 59..269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY03245 standard; Protein; 128 AA.
                                                                                                                   gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                            99US-0122487
06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC03764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 KKRVDHC 42
                                                                                       Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKRIMHC 7
                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                         26-FEB-1999;
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                     EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1999
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Best Loc Matches

ò g RESULT 13 AAY03245

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Gaps

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Search completed: November 1, 2002, 14:47:06 Job time : 3.58682 secs
N-PSDB; AAT18037
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                                                                                                                                                                                                                   New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "corresponds to bovine thymus FKBP-13 N-terminal sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting anglogenesis and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                             Molenaar AJ;
                                                 (GENE-) GENESIS RES & DEV CORP LTD.
(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2
Pred. No. 64;
1; Mismatches
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                                                                                                                             Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..21
/label= sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR93551 standard; Protein; 141 AA
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                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 80; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
  99US-0150330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               920S-0822966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burakoff SJ,
                                                                                                                          Gleen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22..61
                                                                                                                                                                            WPI; 2001-226619/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111: 11
43 KKRVDHC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKRIMHC 7
                                                                                                                          Havukkala IJ,
  23-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5498597-A
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  Db
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The FKBP-13 protein may be used for identifying immunosuppressant drugs, and may be used in combination with immunosuppressant drugs for therapeutic purposes in the treatment of autoimmune disease e.g. rheumatoid arthritis and type-I diabetes, organ transplant and graft versus host disease. The recombinant form of the protein could be potentialler and therefore easier to introduce into cells than intact FKBP-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Purified mammalian FKBP-13 polypeptide capable of binding FK506 useful for identifying and studying immunosuppressant drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                           Claim 1; Fig.1; 12pp; English.
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                   141 AA;
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; 0

OM protein

Run on:

Sequence:

Searched:

Database

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A Bulach D.W., Kumar C.A., Zaia A., Liang B., Tribe D.E.;
Bulach D.W., Kumar C.A., Zaia A., Liang B., Tribe D.E.;

"Group II Nucleopolyhedrovirus Subgroups Revealed by Phylogenetic
Analysis of Polyhedrin and DNA Polymerase Gene Sequences.";

L. Submitted (MAY-1998) to the EMBL/Genbank/DDBJ databases.

-!-CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N
PYROPHOSPHATE + DNA(N).

-!-SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

R. FIMEL; AF068186; AAC33749.11; --
Interpro; IPR002064; DNA_POL_B.
R. Pfam: PF001104; DNA_POL_B. 1.
R. Pfam: PF001104; DNA_POL_B. 1.
R. Pfam: PF001106; DNA_POL_B. 2.
R. RAMRT; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 12; Length 636;
Pred. No. 20;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA replication; DNA-binding; DNA-directed DNA polymerase.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spodoptera exigua nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=10454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DNA POLYMERASE (FRAGMENT).
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09YDU2
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Q9PYW7
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Q9XW94
080588
Q943X8
Q20367
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llarity 85.7%;
Conservative
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                                                                                                       69
    NON_TER
SEQUENCE
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    074308 schizosacch
Q9rv8 homo sapten
096143 plasmodium
013348 magnaporthe
Q65625 rattus norv
0991y6 homo sapten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O90142 spodoptera
Q9j844 spodoptera
Q9cy64 mus musculu
Q9dd21 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9bsm2 homo sapien
O9d3r6 mus musculu
O9h8f4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  022019 cyanidiosch
094164 caenorhabdi
                                                                                                                                                                  (without alignments)
952.238 Million cell updates/sec
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                                                                                                                                            November 1, 2002, 14:43:08; Search time 1.45338 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                           562222 segs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
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Q9D3R6
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Q96143
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Q9P1Y6
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                     1 QKLCHQKK 8
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Match 1
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76.1
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Oguces strongyloce Ogxw94 caenorhabdi O80588 arabidopsis O943x8 oryza sativ Q20367 caenorhabdi

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O9sspl arabidopsis

09h497 homo sapien 09h6e7 homo sapien

Q96kv9 homo sapien Q96kw0 homo sapien Q9eug2 escherichia Q97zs9 sulfolobus Q976h5 sulfolobus

Ogcse2 mus musculu Ogh495 homo sapten O21866 caenorhabdi

Ogovta mus sp. mpl. O80631 arabidopsis O17461 caenorhabdi

09h2s0 homo sapien 09ulul homo sapien 09qvt4 mus sp. mpl

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Local Similarity

Best Loca Matches

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Best Local Similarity
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STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
MEDLINE=2108566; PubMed=11217851;
MEDLINE=2108566; PubMed=11217851;
Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukudishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

IJKel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                           MEDLINE-20036646; PubMed-10567663;
LJKel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
                                                                                                                                                                                                                                             "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome."; J. Gen. Virol. 80:3289-3304(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 1063;
                                                                                                                                                                                                                                                                                                                                                      PYROPHOSPHATE + DNA(N).

-1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

EMBL; AF169823; AAF33622.1; -.

Interpro; IPR00204; DNA_pol_B.

Pfam; PF00136; DNA_pol_B; 1.

Pfam; PF00104; DNA_pol_B.

PRINTS; PR00106; DNA_pol_B.

SMART; SM00406; DNA_pol_B.

DNA replication; DNA binding; DNA-directed DNA polymerase.

SEQUENCE 1063 AA; 123109 MW; 471603FAA92B9A10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus
                                                                                               (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
                                                            PRT; 1063 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 AA.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
                                                                                                                                   Spodoptera exigua nucleopolyhedrovirus.
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                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
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                                                                                                                                                                                                                                   Goldbach R.W., Vlak J.M.;
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Best Local Similarity 85./~
For 6; Conservative
                                                            PRELIMINARY;
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                                                                                                                        ORF93 DNA POLYMERASE.
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SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID-10454;
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392 KLCHQKQ 398
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                                                                       09J844;
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                                  RESULT 2
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XX SUCENCE FROM N. A. S. SUCENCINEY;
XX MEDLINE=2108566; PubMed-11217851;
XX MEDLINE=2108566; PubMed-11217851;
XX ARAWA J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito T., Osazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., Ashill P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakri K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Browstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., Anchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithashi H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Myashariaki Y., Vanshi Y., Kawaji H., Rohtsuki S., Nasaki Y., Kawaii H., Rohtsuki S., Nasaki Y., Kawaii H., Rohtsuki S., Nasaki Y., Kawaii H., Kohtsuki S.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Feltcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK010847; BAB27219.1; -.
MGD; MGI:1917355; 2500001NO3Rik.
InterPro; IPR000683; GPC_IDH_MOCA.
Pfam; PF01408; GPC_IDH_MOCA.
SEQUENCE 295 AA; 33524 MW; F2E1682BD77032A4 CRC64;
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Last annotation update)
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MGD; MGI:1915580; 0610006A11Rik.
InterPro; IPR000683; GFO_IDH_MocA.
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62.58;
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Matches 5; Conservative
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288.QRLCHRKQ 295
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01-JUN-2001
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Kawai J., Shinggawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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Subtaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae: Musinae: Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 34.9 KDA PROTEIN (FRAGMENT).
HOMO sapiens (Human).
HOMO sapiens (Homan).
HOMO Sapiens (Homo).
HOMO Sapiens (Homo).
HOMO Sapiens (Homo).
HOMO Sapiens (Homo).
                                                                                                                                                                                       73.9%; Score 34; DB 5; Length 208; 83.3%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO049550; AAH04950.1; -.
             InterPro; PR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
SMART; SM00131; KU; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00299; BPTI_KUNITZ_2; 1.
Hypothetical protein; Serine protease inhibitor.
SEQUENCE 208 AA; 24008 MW; 779AB4AB948E67B0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 322 AA
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                                                                                                                                                                                                                                   1; Mismatches
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MEDLINE-21085660; PubMed-11217851;
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
4933439B08RIK PROTEIN.
EMBL; U70857; AAB09170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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                                                                                                                                                                                                         t Local Similarity
ches 5; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                              3 ГСНОКК 8
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NCBI_TaxID=6239;
Gaps
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  Indels
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Blanchard M., Bradshaw H.;
"The sequence of C. elegans cosmid Cl0G8.";
submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03144; GTP_EFTU_D2; 1.
Prodom; PD186100; IF2; 1.
PROSITE; PS01118; SU11_1; UNKNOWN_1.
SEQUENCE 420 AA; 47691 MW; A6CAE107B24B4E19 CRC64;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
NCBI_TaxID-45157;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 34;
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Ohta N.;
J. Plant Res. 110:235-245(1997).
EMBL; D63675; BAA22815.1; -.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR00178; IF2.
InterPro; IPR001956; SUII.
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85.7%;
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Science 282:2012-2018(1998).
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Conservative
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                                                                   1:111:1:
288 QRLCHRKQ 295
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236 QKLCHPK 242
                                        1 QKLCHQKK 8
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Matches
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Milming L., Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
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JESSUE-FLACENTA.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isonase T., Nomira Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK023741; BAB14663.1;

InterPro; IPR001849; PH.

InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                        73.9%; Score 34; DB 11; Length 409; 83.3%; Pred. No. 52;
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                                                                                                                                                                                                                                                 409 AA; 46131 MW; 9600B2000BDC9749 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   09H8F4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ13679 FIS, CLONE PLACE2000006.
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                                                                                                                                              Nature 409:689-690(2001).
EMBL, AK017114; BAB30604.1;
MGD, MGI:1918456; 4933439B08Rik.
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
SMART; SM00382; AAA; 1.
ATP-binding.
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SEQUENCE 522 AA; 59222 MW;
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Pfam; PF00621; RhoGEF; 1.
SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conserv
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122 KICHQK 127
                                                                                                                                                                                                                                                                                                                        2 KLCHQK 7
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                                                                                                                                                                                                                                                                         Query Match
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Q9H8F4
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RESULT 10

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InterPro; IPR01138; Zn2_CY6_fungal.
Pfam; PF00172; Zn_clus; 1.
SMART; SM0006; GAL4; 1.
PROSTTE; PS00463; ZN2_CY6_FUNGAL_1; 1.
PROSTTE; PS50048; ZN2_CY6_FUNGAL_2; 1.
DNA-binding; Metal-binding; Nuclear protein; Transcription regulation;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Gaillardin C.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE BINUCLEAR CLUSTER DOMAIN.
EMBL; AL031349; CAA20477.1; -
HSSP; P25502; 12ME.
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Pred. No. 67;
2; Mismatches 0; Indels
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Pred. No. 94;
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                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                         08, Created)
08, Last sequence update)
19, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
547 AA.
                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
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   PRT;
                                                   01-NOV-1998 (TrEMBLrel. 08, Creat. 01-NOV-1998 (TrEMBLrel. 08, Last. 01-DEC-2001 (TrEMBLrel. 19, Last. HYPOTHETICAL ZINC-FINGER PROTEIN. SPBC15D4.02.
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71.48;
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62.5%;
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InterPro; IPR000219; RhoGEF.
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Pfam; PF00621; RhoGEF; 1.
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les 5; Conservative
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PRELIMINARY;
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427 RKLCHEK 433
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MEDLINE=99021743; PubMed=9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Gardner M.J., Tettelin B., Mason T., Yu K., Fujil C., Pederson J.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujil C., Pederson J.,
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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   Gaps
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"Magnaporthe grisea repeated DNA element MGR583 is a member of the
LINE-1 class of polyA retrotransposons.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF018033; AAB71689.1;
InterPro: IPR002156; RNaseH.
InterPro: IPR000477; RVTSe.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                         Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.9%; Score 34; DB 5; Length 1188; Best Local Similarity 71.4%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 0; Indels
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SEQUENCE 1295 AA; 144308 MW; E811059B750D5421 CRC64;
   Indels
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                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PROTEIN WITH 5'-3' EXONUCLEASE DOMAIN (KEM-1 FAMILX)
PFB02055C
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013348;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
REVERSE TRANSCRIPTASE.
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                                                                                                                                                      PRT; 1188 AA.
 3; Mismatches
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Pfam; PF00078; rvt; 1.
5; Conservative
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1117 EELCHQK 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20277482; PubMed-10819331;
MEDLINE-20277482; PubMed-10819331;
Nagase T., Kikuno K., Ishikawa K., Hirosawa M., Ohara O.;
Nagases T., Kikuno K., Ishikawa K., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human
genes. XVII. The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro.";
DNA Res. 7.143-150(2000).
BEMBL; AB040975; BAA96066.1; -.
HSSP; P28990; 1CHC.
                                                                                                                                                                                                                                                                                                                                                                 "The Creminal domain of the largest subunit of RNA polymerase II interacts with a novel set of serine/arginine-rich proteins."; proc. Natl. Acad. Sci. U.S.A. 93:6975-6980(1996).

EMBL: U4057; AAC52658.1; ---
SEQUENCE 1473 AA: 161204 MW; 949EE6F5873989BF CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                 MEDLINE-96293459; Pubmed-8692929;
Yuryev A., Patturajan M., Litingtung Y., Joshi R.V., Gentile C.,
Gebara M., Corden J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.9%; Score 34; DB 11; Length 1473; 71.4%; Pred. No. 1.6e+02; Live 1; Mismatches 1; Indels
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                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIAA1542 PROTEIN (FRAGMENT).
                                                                                              PRT; 1473 AA
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INCEPTO: IPRO01965; PHD_
INCEPTO: IPRO01965; PHD_
INCEPTO: IPRO01961; Znf_ring.
Ffan; PFO0628; PHD; 1.
SWART; SW00109; C1; 1.
SWART; SW00149; PHD: 1.
SWART; SW00184; RING; 2.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
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                                                                                              PRELIMINARY;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=HIPPOCAMPUS;
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|1425 QKICHSK 1431
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33 ELCHQRK 39
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Q9P1Y6
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Query Match 73.9%; Score 34; DB 4; Length 1654; Best Local Similarity 71.4%; Pred. No. 1.8e+02; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Matches 5; Conservative 1; Mis Qy 1 QKLCHQK 7 ||:|| | Db 1606 QKICHSK 1612 Search completed: November 1, 2002, 14:49:49 Job time: 4.45338 secs

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MCCOURTEY W.K. Jr., Maines M.D.;

Title-directed mutagenesis of cysteine residues in biliverdin stitle-directed mutagenesis of cysteine residues in biliverdin stitle-directed mutagenesis of cysteine residues in biliverdin reductase. Roles in substrate and cofactor binding.";

L. Bucchem. 222.597-603(1994).

- !- FUNCTION: CONVERTS BILIVERRIN TO BILIRUBIN: DISPLAYS TWO DISTINCT CHONTON: CONVERTS BILIVERRIN TO BILIRUBIN: DISPLAYS TWO DISTINCT

- !- FUNCTION: CONVERTS BILIVERRIN TO BILIRUBIN: HOMEVER, IS THE PROBABLE COPACTOR IN BILILUBIN + NAD(P)(+) - biliverdin + NAD(P)H.

- !- CATALYTIC ACTIVITY: BILIRUBIN + NAD(P)(+) - biliverdin + NAD(P)H.

- !- PATHWX: FINAL STEP IN HEME METABOLISM.

- !- SUBUNIT: WONOMER (BY SIMILARITY).

- !- SUBUNIT: TO E.COLI YHHX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fakhrai H., Maines M.D.;
"Expression and characterization of a cDNA for rat kidney biliverdin reductase. Evidence suggesting the liver and kidney enzymes are the same transcript product.";
3. Biol. Chem. 267:4023-4029(1992).
                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattua.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UDL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
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Q01767
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TISSUE-Kidney;
MEDLINE-92156147; Pubmed-1371282;
                                        GAG_VILV2
GAG_VILVK
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LAT_STRCL
CAPB_BACAN
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InterPro; IPR000683; GFO_IDH_MOCA.
Oxidoreductase; NAD; NADP; Zinc.
PROPEP 1 295
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Copyright (c) 1993 - 2002 Compugen Ltd
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YO81_CAEEL
SYI_MYCGE
AT12_HUMAN
EX7S_BACSU
NEUT_BOVIN
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2145_HUMAN
VE6_PAPVE
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processing
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O05516:
             SEQUENCE
                                                                                                                                              Z145_HUMAN
   mRNA
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                                                                                                                      ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 589-654 FROM N.A.
MEDLINE-90014786; PubMed-2552292;
Liu Y., Dieckmann C.L.;
"Overproduction of yeast viruslike particles by strains deficient in a mitochondrial nuclease.";
Mol. Cell. Biol. 9:3323-3331(1989).
-:- FUNCTION: RESPONSIBLE FOR CONFERRING A STABLE 5'END ON CYTOCHROME
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                      sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of yeast chromosome X.";
Yeast 10:1657-1662(1994).
                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycoties;
                                                                                                                                                                                                                                                                                                                                                                      Dieckmann C.L., Homison G., Tzagoloff A.;
"Assembly of the mitochondrial membrane system. Nucleotide seque of a yeast nuclear gene (CBP1) involved in 5' end processing of cytochrome b pre-mRNA.";
J. Biol. Chem. 259:4732-4738(1984).
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vandenbol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
                                                                                                 100.0%; Score 46; DB 1; Length 295; 100.0%; Pred. No. 0.19;
                                                                                                                      Indels
                                                                 >A: REDUCED ACTIVITY.
219C8EA96C150588 CRC64;
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                      .;
                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Cytochrome B pre-mRNA processing protein 1.
                                                                                                                                                                                                                      654 AA.
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                    CBP1 OR YJL209W OR J0242 OR HRA654.
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 259:4732-4738(1984).
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-84185566; PubMed-6325407;
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EMBL; Z34098; CAA84002.1; -.
EMBL; Z49484; CAA89506.1; -.
EMBL; M28067; AAA3456.1; -.
PIR; S05829; BVBYP1.
                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
                                                                            33565 MW;
                                                                                                                       Conservative
                                                                                                                                                                                                                      STANDARD;
                      291
                     291
292
73
280
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295 AA;
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                                                                                                          Local Similarity
                                                                                                                                                                288 QKLCHQKK 295
                                                                                                                                           1 OKLCHOKK 8
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                                                                                                                                                                                                                    CBP1_YEAST
P07252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilger F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B MRNA.
                                          MUTAGEN
MUTAGEN
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SEQUENCE
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                       METAL
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                                 METAL
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SGD;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; PLFZA AND PLZFB (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WITHIN THE HEMANOPOLETIC SYSTEM, PLZF IS
EXPRESSED IN BONE MARROW, EARLY MYELOID CELL LINES AND PERIPHERAL
BLOOD MONONUCLEAR CELLS: ALSO EXPRESSED IN THE OVARY, AND AT LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rearrangements of the retinoic acid receptor alpha and promyelocytic leukemia zinc finger genes resulting from t(11;17)(q23;q21) in a patient with acute promyelocytic leukemia."; J. Clin. Invest. 91:2260-2267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Structure-function studies of the BTB/POZ transcriptional repression
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. MAY PLAY A ROLE IN MYELOID MATURATION AND IN THE DEVELOPMENT AND/OR MAINTENANCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY RETINOIC ACID.
DISEASE: A FORM OF ACUTE PROMYELOCYTIC LEUKEMIA (APL) IS
CHARACTERIZED BY A CHROMOSOWAL TRANSLOCATION T(11:17) (032;021)
WHICH INVOLVES 2NF145 AND RETINOIC ACID RECEPTOR ALPHA (RARA).
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93253074; PubMed-8387545;
Chen S.-J., Zelent A., Tong J.-H., Yu H.-Q., Wang Z.-Y., Derre J.,
Berger R., Waxman S., Chen Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20005701; PubMed=10537309;
Li X., Peng H., Schultz D.C., Lopez-Guisa J.M., Rauscher F.J. III,
Marmorstein R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YESUBNCE FROM N.A.
TISSUB-Heart ventricle;
MEDLINE-93209216, PubMed-8384553;
Chen Z., Brand N.J., Chen A., Chen S.-J., Tong J.-H., Wang Z.-Y.,
Waxman S., Zelent A.;
Firston between a novel Kruppel-like zinc finger gene and the
rethionic acid receptor-alpha locus due to a variant t(11:17)
translocation associated with acute promyelocytic leukaemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain from the promyelocytic leukemia zinc finger oncoprotein.";
Cancer Res. 59:5275-5282(1999).
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01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Zinc finger protein PLZF (Promyelocytic leukemia zinc finger protein) (Zinc finger protein 145).
NF145 OR PLZF.
Homo sapiens (Human).
654 AA; 76171 MW; 2453B03280E1C44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 7-122.
                                                                    DB 1;
                                                                                                     23;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                    Score 36;
                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEVELS, IN THE KIDNEY AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER DIFFERENTIATED TISSUES.
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                                                                    78.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 12:1161-1167(1993).
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                    Query Match
Best Local Similarity
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European elk papillomavirus (EEPV).";
Gene 50:195-205(1986).
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                                                                                                                                                                                                                                                                                                                                                         EMBL; M15953; AAA66849.1; -.
                                                                                                STRANDED DNA (IN VITRO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                  PIR; A29499; W6WLEP.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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24 KRCHEKK 30
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23 KNLCHQK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQS3_CAEEL
Q09311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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YQS3_CAEEL
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                          R InterPro; IPR000210; BTB_POZ.

R InterPro; IPR000822; Znf-C2H2.

R Pfam; PF000651; BTB; 1.

R PRINTS; PR00048; ZINCFINGER.

SMART; SM00225; BTB; 1.

SMART; SM00325; BTB; 1.

R PROSITE; PS00097; BTB; 1.

R PROSITE; PS00029; ZINC_FINGER_C2H2_1; 8.

R PROSITE; PS00029; ZINC_FINGER_C2H2_2; 9.

R PROSITE; PS00029; ZINC_FINGER_C2H2_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-87219878; PubMed-3034730; Ahola H., Bergman P., Stroem A.C., Moreno-Lopez J., Petterson U.; "Organization and expression of the transforming region from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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01-JUL-1989 (Rel. 11, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
E6 protein.
E6.
European elk papillomavirus (EEPV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC FINGERS
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                EMBL; Z19002; CAA79489.1; -. EMBL; S60093; AAC60590.2; -.
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                                                                                                                                                                                                            PDB; 1CS3; 09-AUG-00.
TRANSFAC; T02336; -.
MIM; 176797; -.
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184
197
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673 AA;
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461
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P11331;
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MOD_RES
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VARSPLIC
SEQUENCE
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ZN_FING
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-! - FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
Early protein; DNA-binding; Nuclear protein; Zinc-finger.
ZN_FING 11 47 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 23.6 kDa protein F21H12.3 in chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA; 15869 MW; AE4F1BABC95E0459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 210 AA; 23617 MW; 1E646E6FC30154A0 CRC64;
                                                                   -! - SUBCELLULAR LOCATION: Nuclear matrix-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.6%; Score 32; DB 1; 71.4%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QKLCHQK 7
                                                                                                                                                                                                                               STRAIN=CPN50;
                                                                                                                                              flesh-eater.
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P29055;
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                        Elsemore D.A., Ornston L.N.;
"Unusual ancestry of dehydratases associated with quinate catabolism in Acinetobacter calcoaceticus.";
J. Bacteriol. 177:5971-5978[1995].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO DEHYDROSHIKIMATE.

--- CATALYTIC ACTIVITY: 3-dehydroquinate - 3-dehydroshikimate + H(2)0.

--- PATHWAY: OUINIC ACID CATABOLIC PATHWAY; SECOND STEP. THIS PATHWAY ALLOWS GROWTH OF BACTERLA WITH QUINATE BY ITS CONVERSION TO PROTOCATECHUATE AND SUBSEQUENT METABOLISM BY THE BETA-KETOADIPATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Clostridium perfringens.
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMS A SCHIFF-BASE INTERMEDIATE (BY SIMILARITY). 98646DC5E88BF6D3 CRC64;
                                                                                                                                                                                                                          Acinetobacter calcoaceticus.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 272;
                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catabolic 3-dehydroquinate dehydratase (EC 4.2.1.10) (3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
55;
                                                           272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION. STRAIN-BD413 / ADP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L05770; AAC37158.1; ALT_INIT.
InterPro: IPRO01381; DHquinase_I.
Pfam; PF01487; DHquinase_I: 1.
PROSITE; PS01028; DEHYDROOUINASE_I: 1.
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: BY PROTOCATECHUATE.
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96011389; PubMed=7592351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quinate metabolism; Lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                  dehydroquinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 KLAHOKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                 Acinetobacter.
NCBI_TaxID=471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KLCHOKK 8
                                                                                               16-OCT-2001
16-OCT-2001
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Q46185;
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                                                           3DHQ_ACICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                      3DHQ_ACICA
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                                                                                                                                                                                                                                                                                                              Katayama S.-I., Dupuy B., Garnier T., Cole S.T.;
"Rapid expansion of the physical and genetic map of the chromosome of Clostridium perfringens CPN50.";
J. Bacteriol. 177:5680-5685(1995).
-:- CATALYTIC ACTYVITY: LL-2,6-diaminoheptanedioate - mesodiaminoheptanedioate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF LYSINE FROM ASPARTATE SEMIALDEHYDE.
                                                                                        Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
11-DEC-1998 (Rel. 36, Last annotation update)
Transcription initiation factor IIB (TFIIB) (Transcription factor SUA7 OR YPRO86W OR P9513.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE DIAMINOPIMELATE EPIMERASE FAMILY.
-1- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 181.
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                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
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                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X86511; CAA60229.1; ALT_FRAME. HSSP; P44859; 1BWZ.
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                                                                                                                                                                                                                               SEQUENCE OF 168-238 FROM N.A.
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STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 AA;
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                                                                                                                                                                                                                                                                                   PubMed=7559358;
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32 QKMCHRR 38
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PRIM_CHLTR
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         HAD DE TANKER BY AND THE STREET T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                              SEQUENCE FROM N.A.

STRAIR=S286C / AB972;

STRAIR=S286C / AB972;

STRAIR=S286C / AB972;

STRAIR=S286C / AB972;

SANCE AB972;

Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,

Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

Johnston D., Johnston L., Larreille P., Le T.,

Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,

Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,

Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;

Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.

-I- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
                         Pinto I., Ware D.E., Hampsey M.; "The yeast SUA7 gene encodes a homolog of human transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                              OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II.
-!- SUBUNIT: ASSOCIATES WITH TFIID-IIA (DA COMPLEX) TO FORM TFIID-
IIA-IIB (DAB-COMPLEX) WHICH IS THEN RECOGNIZED BY POLYMERASE II.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE TFIIB FAMILY.
                                                                TFIIB and is required for normal start site selection in vivo. Cell 68:977-988(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0782; TFIIB; 1.
Transcription regulation; Nuclear protein; Repeat; Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 1; Length 345;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA; 38200 MW; 8F1F6D24602436E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00382; transcript_fac2; 2.
PRINTS; PR00685; TIFACTORIIB.
SMART; SM00385; CYCLIN; 2.
MEDLINE-92191276; PubMed-1547497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0006290; SUA7.
InterPro; IPR000553; Cyclin.
InterPro; IPR000812; TFIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; W81380; AAA35126.1; -. EMBL; U51033; AAB68135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.68;
71.48;
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Best Local Similarity 71.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U51033; AAB6813;
PIR; S26707; S26707.
HSSP; Q00403; 1DL6.
TRANSFAC; T00819; -.
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242
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P47545;
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MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĄŢ
                                                    Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidhan J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nuyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M. Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL RNA PRIMERS FOR THE OKAZAKI FRACMENTS ON BOTH TEMPLATE STRANDS REPLICATION FORKS DURING CHROMOSOMAL DNA SYNTHESIS.
-!- COPACTOR: BINDS ONE ZINC ION PER MOLECULE (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00211; ABC_TRANSPORTER; FALSE_NEG.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
NP_BIND 107 114 ATP (POTENTIAL).
SEQUENCE 357 AA; 40786 MW; AFB1012F886E090E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA primase (EC 2.7.7.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%; Score 32; DB
83.3%; Pred. No. 69;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003439; ABC_transportr.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPRO01687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U39710; AAC71525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONAG OR CT794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGR; MG303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIM_CHLTR
084799:
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                         Primosome;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEOMBLES 9:66-72(1991).

-1- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND BILINGUIN: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND BILINGUIN LESS WELL THAN, SERUM ALBUMIN.

-1- SUBUNIT: DIMERIC FORM (BY SIMILARITY).

-1- STBCELLULAR LOCATION: Extracellular.

-1- TISSUE SPECIFICITY: PLASAA.

-1- DOMAIN: COMPOSED OF THREE HOWLOGGUS DOMAINS.

-1- PTM: SULFATED (BY SIMILARITY).

-1- PTM: SULFATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91169517; PubMed-1706310;
Ryan S.C., Ziellnski R., Dugaiczyk A.;
"Structure of the gorilla alpha-fetoprotein gene and the divergence
of primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                           H HSSP: 09X4D0; 1D00.

R InterPro; IPR002936; Toprim.

R InterPro; IPR00294; ZnF_CHCC.

R Pfam; PF01/51; Toprim; 1.

R ProDom; PF01/51; Toprim; 1.

R SMART; SM00409; ZnF_CHCC; 1.

R SMART; SM00400; ZnF_CHCC; 1.

R SMART; SM00400; ZnF_CHCC; 1.

R Transferase; DNA replication; DNA-directed RNA polymerase; Prin Transferase; DNA replication; DNA-directed RNA polymerase; Prin ZnC; Metal-binding; Complete proteomer.

R ZNFING 38 62 CHC2-TYPE (BY SIMILARITY).

SEQUENCE 595 AA; 68037 MW; 536858EBAFCD8FB6 CRC64;
                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                       Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
                                                                                                                                                                                                                                    69.6%; Score 32; DB 1; Length 595
83.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 609 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorilla gorilla gorilla (Lowland gorilla).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P02768; 1BJ5.
InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD002486; Serum_albumin; 1.
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                    EMBL; AE001351; AAC68389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M38272; AAA73520.1; -.
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9595;
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565 RKLCHQ 570
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                                                                                                                                                                                                                                                                                                                                                                               FETA_GORGO
P28050;
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87185438; PubMed-2436661;
Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczyk A.;
Structure, polymorphism, and novel repeated DNA elements revealed
a complete sequence of the human alpha-fetoprotein gene.";
Biochemistry 26:1332-1343(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 . .) (POTENTIAL)
                                                                                                            SIMILARITY)
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Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
"Primary structures of human alpha-fetoprotein and its mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein)
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 2.
Glycoprotein; Sulfation; Albumin; Plasma; Embryo; Repeat;
Metal-binding; Copper; Nickel; Signal.
SIGNAL BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (PC E8AE548377DB60EB CRC64;
                                                                                     ALPHA-FETOPROTEIN.
COPPER AND NICKEL (BY S
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.1e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Genet. 2:379-379(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                    MM;
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                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                  609 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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96 EELCHEKE 103
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P02771;
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                                                                                           CHAIN
                                                                                                            METAL
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us-09-606-129a-19.rsp

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DEVELOPMENTAL STAGE: OCCURS IN THE PLASMA OF FETUSES MORE THAN 4 WEEKS OLD, REACHES THE HIGHEST LEVELS DURING THE 12TH-16TH WEEK OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
-!- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACLDS AS WELL AS, AND
BILIRUBIN LESS WELL THAN, SERUM ALBWIN, ONLY A SMALL PERCENTAGE
(LESS THAN 28) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Alpha fetoprotein: structure and expression in man and inbred mouse strains under normal conditions and liver injury."; Johns Hopkins Med. J. Suppl. 3:249-255(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-80001710; PubMed-89900;
Aoyaqi Y., Ikenaka T., Ichida F.;
"Alpha Fetoprotein as a carrier protein in plasma and its bilirubin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION TO THE MONOMERIC FORM.
SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                      MEDIINE=77242506; PubMed=70228; Yachnin S., Hsu R., Heinrikson R.L., Miller J.B.; "Studies on human alpha-fetoprotein. Isolation and characterization of monomeric and polymeric forms and amino-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                               from
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                                                                                      PARTIAL SEQUENCE OF 19-609.
MEDLINE=91243409; PubMed=1709810;
Pucci P., Siciliano R., Malorni A., Marino G., Tecce M.F.,
Ceccarini C., Terrana B.;
"Human alpha-fetoprotein primary structure: a mass spectrometric
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-78001760; PubMed-71198;
Aoyaqi Y., Ikenaka T., Ichida F.;
"Comparative chemical structures of human alpha-fetoproteins from
fetal serum and from ascites fluid of a patient with hepatoma.";
Cancer Res. 37:3663-3667(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The human alpha-fetoprotein gene. Sequence organization and the
Beattie W.G., Dugaiczyk A.; "structure and evolution of human alpha-fetoprotein deduced from "structure and evolution of partial sequence of cloned cDNA."; Gene 20:415-422(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 19-39.
MEDLINE-75018719; Pubmed-4138095;
Ruoslahti E., Pihko H., Vaheri A., Seppala M., Virolainen M.,
Konttinen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakai M., Morinaga T., Urano Y., Watanabe K., Wegmann T.G., Tamaoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=79001617; PubMed=80265;
AGVAG1 Y., Ikenaka T., Ichida F.;
"Copper(II)-binding ability of human alpha-fetoprotein.";
Cancer Res. 38:3483-3486(1978).
                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 493:418-428(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flanking region.";
J. Biol. Chem. 260:5055-5060(1985)
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Cancer Res. 39:3571-3574(1979).
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GESTATION, AND DROPS TO TRACE AMOUNTS AFTER BIRTH. THE SERUM LEVEL
        IN ADDLTS IS USUALLY LESS THAN 40 NG/ML. AFP OCCURS ALSO AT HICH LEVELS IN THE PLASMA AND ASCITIC FLUID OF ADDLTS WITH HEPATOMA. DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

PTW: INDEPENDENT STUDIES SUGGEST HETEROGENEITY OF THE AMINOTERMINAL SEQUENCE OF THE MATURE PROTEIN AND OF THE CLEAVAGE SITE OF THE SIGNAL SEQUENCE.

PTM: SULFATED.

SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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Glycoprotein; Sulfation; Albumin; Plasma; Embryo; Repeat;
Metal-binding; Copper; Nickel; Signal; Polymorphism.
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A -> G (IN DBSNP:1057173).
/FTId=VAR_012049.
4D4E45820E1C2D4F CRC64;
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Pred. No. 1.1e+02;
4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR00264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
                                                                                                                                                                                                                                        EMBL; M10949; AAAS1674.1; --
EMBL; M10950; AAAS1675.1; --
EMBL; V01514; CAA24758.1; --
EMBL; M16110; AAB58754.1; --
EMBL; J00077; AAC95396.1; --
EMBL; A21933.2; CAA79592.1; --
PIR; A26624; A26624.
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ilarity 50.0%;
Conservative
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GlycoSuiteDB; P02771; -.
Siena-2DPAGE; P02771; -.
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Best Local Similarity
Matches 4; Conserv
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RESULT 13 YO81_CAEEL œ

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Mycoplasma genitalium.
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J. Bacterio
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P58397;
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ID AT12_HU
AC P58397;
DT 01-MAR-
DT 01-MAR-
DT 01-MAR-
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                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copesy T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latrellle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Suns M., Smaldon N., Smith A., Sonhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Wateston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
LEPA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                   "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                      01-FEB-1994 (Rel. 28, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Hypothetical GTP-binding protein ZK1236.1 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 645;
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Pred. No. 1.2e+02;
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GTP (POTENTIAL).
GTP (POTENTIAL).
 645 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
Pfam; PF001009; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
PRT;
                                                                                                                                                          STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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165 GT
; 72268 MW;
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75.08;
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 STANDARD;
                                                                                   Caenorhabditis elegans,
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Best Local Similarity
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SEQUENCE FROM N.A.
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614 KKLSHQKK 621
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ILES OR MG345.
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 YO81_CAEEL
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P47587;
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                              Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Wlayton D.T., Utterback F.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00964; TRNASYWHILE.
PROSITE; PS00178; AA_TRNA_LIGSE_1; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 262-371 AND 605-711 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
PEPERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 175:7918-7930(1993).
-!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP diphosphate + L-isoleucyl-tRNA(Ile).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ing; Zinc; Complete proteome.
57 67 "HIGH" REGION.
59 594 "KMSKS" REGION.
593 593 ATP (BY SIMILARITY).
895 AA: 104395 MW; 8C78DE6A05311B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002300; tRNA-synt_la.
Interpro; IPR001412; tRNA-synt_I
Interpro; IPR002301; tRNA-synt_ile.
                                                                                                                        SEQUENCE FROM N.A.
STRAIN=AFCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                      Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U39716; AAC71570.1; -. EBML; U02196; AAD12482.1; -. EMBL; U02254; AAD12519.1; -. HSSP; P41972; 1FFY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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nes 5; Conserv
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122 RKLCHQ 127
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                                                                                                                                                                                                                                                                                                      origin.
DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE I DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                              MATRIX (BY SIMILARITY).
TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is widely
                                                                                                                                                                Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.; "Identification, characterization, and intracellular processing of ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats."; J. Blol. Chem. 276:17932-17940(2001).
-: COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-: SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                           PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND
TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALOPROTEINASE, DISSINTERRIN-LIKE, CYS-RICH AND TS-1 DOMAINS
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
ADAWTS-12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM
                                                                                                                                                                                                                                                                                          expressed in gastric carcinomas and in cancer cells of diverse
                                                Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 606184; -...
PROSTTE; PS50215; ADAM_MEPRO; 1.
PROSTTE; PS00427; DISINTEGRIN_1; FALSE_NEG.
PROSTTE; PS00422; TSP1; 2.
PROSTTE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
-i- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISINTEGRIN-LIKE.
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(CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ADAMTS-12.
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TSP TYPE-1 2.
TSP TYPE-1 4.
SPACER 2.
TSP TYPE-1 5.
TSP TYPE-1 5.
TSP TYPE-1 6.
TSP TYPE-1 7.
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CYS-RICH.
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                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Fetal lung;
MEDLINE=21264577; PubMed=11279086;
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SIGNAL 1 25
PROPEP 26 240
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881
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METAL
                                         ADAMTS12
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Pred, No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07F9F48E63BD83A3 CRC64;
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N-LINKED
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1275
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Matches 5; Conserv
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873 QKKCHEK 879
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Search completed: November 1, 2002, 14:47:48 Job time : 2.41158 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:43:58; Search time 0.848875 Seconds Run on:

(without alignments) 905.569 Million cell updates/sec

US-09-606-129A-19 46 1 QKLCHQKK 8 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sednence:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	46	100.0	295	7	A42268	biliverdin reducta
7	36	78.3	654	Н	BVBYP1	CBP1 protein - yea
e	34	73.9	208	7	E89046	protein C10G8.2 [1
4	34		547	~	T39478	zinc-finger protei
2	34		1188	7	A71621	protein with 5'-3'
9	34		1295	a	T30528	reverse transcript
7	34	73.9	1473	~	T31422	C-terminal domain-
80	33		263	7	E72675	hypothetical prote
6	33	71.7	467	7	AF3147	ທ
10	33	71.7	476	~	D98140	hypothetical prote
11	33	71.7	673	7	836336	⊂
12	33		773		T00554	hypothetical prote
13	33		1247		T18671	
14	32		135		W6WLEP	
15	32		210	7	116125	
16	32		221		D90195	
17	32		290	7	I39522	⊏
18	32		345	٦	S26707	transcription init
19	32		357	7	E64233	membrane transport
20	32		380	7	T24081	hypothetical prote
21	32		422	7	E96753	
22	32		462	7	A46170	S
23	32		465	7	T27032	
24	32		474	7	T00699	
25	32		548	7	T22137	hypothetical prote
26	32		581	7	S44896	$\boldsymbol{\omega}$
27	32		595	~	F71471	probable DNA prima
28	32	9.69	609	~+	FPHU	alpha-fetoprotein
53	32		609		FPGO	alpha-fetoprotein

895 2 B64238 920 2 JC7313 1056 2 JC7313 170 1 UNDG 251 2 G86368 251 2 G86368 251 2 G86368 276 2 J A75401 273 2 A75401 343 2 A75401 343 2 A75401 343 2 A7605 364 2 D84782 478 2 C71523 491 2 G83850	isoleucinetRNA l aryl hydrocarbon r hynorhotical profe	exodeoxyribonucles neurotensin precur	hypothetical prote hypothetical prote	hypothetical prote ribulose-phosphate	probable phosphohy B. subtilis comG o	B. subtills comG o hypothetical prote	probable proline t	probable Shikimate ATP-dependent DNA
2000 2000 2000 2000 2000 2000 2000 200	B64238 JC7313	H69960 UNDG	G86368 T33411	T16421 A75401	G97141 AB1243	AF1605 T03892	D84782	C/1323 G83850
	395 2 320 2	54 2	251 2 266 2	271 2 299 2	324 2 343 2	343 2	136 2	191 2
	32	31	31	31	31	31	31	31
32233333333333333333333333333333333333	30 31 32	9 9 9 1 1 6 9 1	35 36	37 38	39 40	41	43	4 5

ALIGNMENTS

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C; Accession: A42268
B; Fakhrai, H.; Maines, M.D.
J. Biol. Chem. 267, 4023-4029, 1992
A; Title: Expression and characterization of a cDNA for rat kidney biliverdin reductas A; Reference number: A42268; MUID: 92156147
A; Accession: A42268
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid; protein
A; Residues: 1-295 <FAKS
A; Cross-references: GB_MB1681; NID: 9203177; PIDN: AAA40830.1; PID: 9203178
                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIP:82800) C;Keywords: liver; oxidoreductase
biliverdin reductase (EC 1.3.1.24) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: kidney
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Score 46; DB 2; Length 295; Pred. No. 0.51; Indels ö Mismatches ;; Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0;

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Gaps

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1111111 288 QKLCHQKK 295 1 QKLCHQKK 8 8 δλ

CBPI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein HAR654; protein J0242; protein YJL209w
C;Species: Saccharomyces cerevision 31-Mar-1991 #text_change 12-Nov-1999
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Nov-1999
C;Accession: S08829; S56076; S56996; S56996; S45164
R;Dieckmann, C.L.; Honnison, G.; Tzagoloff, A.
J. Biol. Chem. 259, 4732-4738, 1984
A;Title: Assembly of the mitochondrial membrane system. Nucleotide sequence of a yeas A;Reference number: S05829; MUID:84185566 RESULT 2

A; Molecule type: DNA

A; Cross-references: EMBL: Z34098; NID: 9496934; PIDN: CAA84002.1; PID: 9496953

Gaps

; 0

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protein with 5'-3' exonuclease domain (Kem-1 family) PFB0205c - malaria parasite (Pla C: Species: Plasmodium falciparum C; Decies: Plasmodium falciparum C; Decies: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C: Accession: A71621 Fettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H Science 282, 1126-1132, 1998 A.Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A.Reference number: A71600; MUID:99021743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reverse transcriptase - rice blast fungus
C;Species: Magnaporthe grisea (rice blast fungus)
C;Species: Magnaporthe grisea (rice blast fungus)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30528
R;Meyn III, M.A.; Farrall, L.; Valent, B.; Chumley, F.G.; Orbach, M.J.
submitted to the EMBL Data Library, August 1997
A;Description: Magnaporthe grisea repeated DNA element MGR583 is a member of the LINE
A;Reference number: 220845
A;Accession: T30528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1188 <GAR>
A;Cross.references: GB:AE001380; GB:AE001362; NID:g3845120; PIDN:AAC71830.1; PID:g384
A;Experimental source: clone 3D7
C;Genetics:
                                                                                                                        A;Cross-references: EMBL:AL031349; PIDN:CAA20477.1; GSPDB:GN00067; SPDB:SPBC15D4.02 A;Experimental source: strain 972h-; cosmid c15D4
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A;Molecule type: DNA
A;Residues: 1.1295 <MEY>
A;Cross-references: EMBL:AF018033; NID:92454620; PID:92454622; PIDN:AAB71689.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2; Length 547;
Pred. No. 1.2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.9%; Score 34; DB 2; bength 1188; Best Local Similarity 71.4%; Pred. No. 2.2e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   A;Map position: 2
C;Superfamily: GAL4 zinc binuclear cluster homology
F;169-206/Domain: GAL4 zinc binuclear cluster homology <GL4>
                                        A,Accession: T39478
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-547 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                            73.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%
                  A; Reference number: 221858
                                                                                                                                                                                                                                                              A; Gene: SPDB:SPBC15D4.02
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Db 1117 EELCHQK 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | | | : |
427 RKLCHEK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QKLCHQK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QKLCHQK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: PFB0205c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-654 <VANA.
A; Residues: 1-654 <VANA.
A; Residues: 1-654 <VANA.
A; Cross-references: EMBL: 249484; NID: 91015590; PIDN: CAA89506.1; PID: 91015591; GSPDB: GNOG R; Purnelle, B.; Coster, F.; Goffeau, A.
R; Purnelle, B.; Coster, F.; Goffeau, A.
A; Reference number: S56977
A; Reference number: S56977
A; Accession: S56996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Reference number: A75000; MID:99069613; PMID:9851916 A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:chr_V; PIDN:AAB09170.1; PID:91572828; GSPDB:GN00023; CESP:C10G8.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994 R;Vandenbol, M.; Durand, P.; Portetalle. D. Hiller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: pre-mRNA processing
A;Note: required for correct 5' terminal processing of cytochrome b pre-mRNA
C;Superfamily: CBP1 protein
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein C10G8.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 59;
1; Mismatches 1; Indels
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54;
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                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 637-654 <PUR>
A; Cross-references: EMBL: Z49484; GSPDB:GN00010; MIPS:YJL209w
C; Genetics:
                                              R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995 A;Reference number: $556835 A;Accession: $55699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: E89046
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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83.3%; Pred. No. 54;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: SGD:CBP1; MIPS:YJL209w
A;Cross-references: SGD:SG003745; MIPS:YJL209w
A;Map position: 10L
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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514 KKLCHYKK 521
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C;Accession: D99140
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2338, 2001
A;Title: Genome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AGR_L_159 [imported] - Agrobacterium tumefaciens (strain C58, Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Tille: Fusion between a novel Krueppel-like zinc finger gene and the retinoic acid A;Reference number: $36336; MUD: 93209216
A;Reference number: $36336; MUD: 93209216
A;Accession: $36336
A;Molecule type: mRNA
A;Residues: 1-673 < CHE>
A;Cross-references: EMBL: 219002; NID: 938517; PIDN: CAA79489.1; PID: 938518
C;Genetics: A;Gene: PLZF
                                       A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL45596.1; PID:g17743315; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE007870; PIDN:AAK88646.1; PID:915158369; GSPDB:GN00170 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
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Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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83.3%; Pred. No. 2.18+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.7%; Score 33; DB 2; Length 467
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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A;Map position: linear chromosome
C;Superfamily: ornithine--oxo-acid aminotransferase
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C;Superfamily: ornithine--oxo-acid aminotransferase
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C;Keywords: zinc finger
F;20-118/Domain: POZ domain homology <POZ>
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Matches 5; Conservative
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A; Residues: 1-476 <KUR>
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220 QKLCHE 225
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        A; Accession: AF3147
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C;Species: Aeropyrum pernix
C;Species: O-aug-1999 #Sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E72675
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glutamate-1-semialdehyde 2,1-aminotransferase hemi. [imported] - Agrobacterium tumefaciens C:Species: AF3147
R:Wood, D.W.: Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. R:Wood, D.W.: Setubal, J.C.; Kaul, R.; Monks, D.; Chen, T.; Levy, R.; Li, M.; McClell Scape, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                  R:Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Scl. US.A. 93, 6975-6980, 1996
A;Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A;Reference number: 221024; MUID:96293459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
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A, Molecule type: DNA
A. Residues: 1-263 < KAW>
A. Cross-references: DBJ:AP000060; NID:g5104188; PIDN:BAA79805.1; PID:g5104490
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-1473 <YUR>
A; Cross-references: EMBL:U49057; NID:g1438533; PID:g1438534; PIDN:AAC52658.1
A; Experimental source: hippocampus
                                                                                                                                                                                                  C-terminal domain-binding protein rA9 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text_change 07-Dec-1999
C;Accession: T31422
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Pred. No. 2.6e+02;
1; Mismatches 1; Indels
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Pred. No. 99;
1; Mismatches 0; Indels
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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258 LCHQKR 263
    ELCHORK 39
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hypothetical protein F21H12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Saccession: T16125
R;Favello, T.
Submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F21H12.
A;Reference number: 218464
A;Accession: T16125
A;Accession: T16125
A;Accession: T16125
A;Residues: 10-TIG VSAV
A;Residues: 1-210 cFAV
A;Residues: 1-210 cFAV
A;Residues: 1-210 cFAV
A;Cross-references: EMBL:U23176; NID:9726404; PID:9726407; PIDN:AAC46715.1; CESP:F21H
A;Experimental source: strain Bristol N2
C;Genetics:
A;Genetics:
A;Genetics: A;Genetics: A;Genetics: A;Introns: 37/3; 62/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F21H12.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European elk
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A.Residues: 1-135 <AHO>
A.COSS-references: GB:MI5953; NID:g333025; PIDN:AAA66849.1; PID:g484015
B.Erikason, A.
unpublished results 1987, cited by GenBank
A.Reference number: A94457
A.Molecule type: DNA
A.Rocession: F94457
A.Molecule type: DNA
A.Residues: 1-135 <AERI>
A.COSS-references: GB:MI5953; NID:g333025; PIDN:AAA66849.1; PID:g484015
B.Petterson, U.
Submitted to GenBank, August 1987
A.Rocession: F94506
A.Rolecule type: DNA
A.Reference number: A94506
A.Rocession: F94506
A.Rocession: F94506
A.Rocession: F94506
A.Rocession: F94506
A.Rolecule type: DNA
A.Reference number: A94506
A.Rocession: F94506
A.Rocession: F94401
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E6 protein - European elk papillomavirus

C;Species: European elk papillomavirus

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-May-2000

C;Accession: A29499; F94457; F94506

R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.

Gene 50, 195-205, 1986

A;Title: Organization and expression of the transforming region from the Eur

A;Reference number: A1567; MUID:87219878
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5; Conservative
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Best Local Similarity
..hes 5; Conserve
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265 KICHQAK 271
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24 KRCHEKK 30
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23 KNLCHOK 29
KLCHOKK 8
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T16125
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                                                                                                                                                                                                                                                                                  hypothetical protein At2g39440 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F12L6.10
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T00554; D84817
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulbuitted to the EMBL Data Library, July 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A;Reference number: 214168
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A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: 1-773 - R0U>
A.Resigues: 1-773 - R0U>
A.Cross-references: EMBL:AC004218; NID:g3355463; PID:g3355473
A.Experimental source: cultivar Columbia
A.Experimental source: cultivar Columbia
B.Ein, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A;Introns: 29/2; 73/2; 108/2; 129/3; 202/2; 265/3; 401/3; 454/1; 466/3; 553/3; 594/2; 64
C;Superfamily: Caenorhabditis elegans hypothetical protein B0240.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84817 A;Status: preliminary
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A;Reference number: 219004
A;Accession: T18671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1247 <WIL>
A;Cossreferences: EMBL:274026; PIDN:CAA98416.1; GSPDB:GN00023; CESP:B0240.2
A;Cossreference: clone B0240
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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75.08;
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Best Local Similarity 75.0v
The 6; Conservative
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Molecule type: DNA
Residues: 1-773 <STO>
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292.168 Million cell updates/sec
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Sequence 9
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB_pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB_pep:*
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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PCT US55-019-4

DCJ-0855-0114-3

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US-07-847-010-17

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US-08-377-309-2
US-09-186-723-2
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US-09-146-580-2
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Maximum Match 100%
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Perfect score:
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Sequence 3, Application US/09186723

Sequence 3, Application US/09186723

Sequence 3, Application US/09186723

GENERAL INFORMATION:

TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS

TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT

FILE REFERENCE: 06727/005002

CURRENT FILLG DATE: 1998-11-05

SARLIER FILLING DATE: 1998-11-05

EARLIER PELLING DATE: 1995-01-24

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 3: SEQ ID NOS: 16

SEQ ID NO 3: LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08377309A
(SERENAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: NECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: NECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: NECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: NAMERICAL OF 1940 AND 1840 AND
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Pred. No. 1.1e+02;
4; Mismatches 0; Indels
US-07-828-700-9
US-08-973-675-2
US-08-972-2704-12
US-08-772-2704-12
US-08-280-690-2
US-09-103-478-23
US-09-103-478-21
US-09-103-478-21
US-09-103-478-25
US-09-103-478-25
US-09-103-931C-21
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US-09-193-931C-22
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
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        TYPE: PRT
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US-08-37-309-6
Sequence 6, Application US/08377309A
Patent No. 595528
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: AN IMMUNSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005001
CURRENT FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09186723

Patent No. 6288034

GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: AN IMMUNSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005002
CURRENT FILENG DATE: 1998-11-05
CURRENT FILING DATE: 1998-11-05
BARLIER APPLICATION NUMBER: 08/377,309
BARLIER FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
TURENT: 389
TYPE: PRT
TYPE: PRT
COGANISM: Homo sapiens
US-09-186-723-6
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GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
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Pred. No. 2.1e+02;
4; Mismatches 0
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Homo sapiens
US-08-377-309-6
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US-09-186-723-6
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PCT-US96-00996-6
Sequence 6, Application PC/TUS9600996
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
NUMBER OF SEQUENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
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50.0%; Pred. No. 1.1e+02;
iive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: PCT/US96/00996
FILING DATE: A-JAN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 5; Le
Pred. No. 1.1e+02;
4; Mismatches 0;
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06727/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELES: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/377,311
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,309
FILING DATE: 24-JAN-1995
CLASSIFICATION NUMBER: 08/377,316
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/505,012
FILING DATE: 21-JULY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,317
FILING DATE: 24-JAN-1995
CLASSIFICATION:
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STRANDEDNESS: not relevant
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50.0%;
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Best Local Similarity کان.ت
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                      4; Conservative
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PCT-US96-00996-6
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Best Local Similarity
Matches 4; Conserv
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COUNTRY: USA
ZIP: 02110-2804
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TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: 15sh & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
STATE: MA
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APPLICANT: Wurgita, Robert A.
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005002
CURRENT APPLICATION NUMBER: US/09/186,723
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 08/377,309
EARLIER FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 590
TYPE: PRT
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  Indels
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: PCT/US96/00996
FILING DATE: PCT/US96/00996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 4;
Pred. No. 3e+02;
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GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/377,309
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,316
FILING DATE: 24-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,317
FILING DATE: 24-JAN-1995
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APPLICATION NUMBER: 08/377,311
FILING DATE: 24-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                      Sequence 2, Application US/09186723 Patent No. 6288034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.6%;
50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
  4; Conservative
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ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-186-723-2
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08377309A
Patent No. 5965528
GENERAL INFORMATION:
APPLICANT: MICHIGATION:
APPLICANT: MICHIGATION:
APPLICANT: MICHIGAN:
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005001
CURRENT APPLICATION NUMBER: US/08/377,309A
CURRENT FILING DATE: 1999-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 3.0
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US96/00996
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 06727/003001
REFERENCE/DOCKET NUMBER: 06727/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
merry (617) 542-8906
                                                                                                                                                        PILING DATE: 24 -JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,317
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,311
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,309
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,316
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/377,316
FILING DATE: 24-JAN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/505,012
FILING DATE: 21-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 389 amino acids TYPE: amino acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.6%;
50.0%;
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-08-377-309-2
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Best Local Similarity
02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QKLCHQKK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US96-00996-9
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LENGTH: 590
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RESULT 12
US-09-002-114-3
Sequence 3, Application US/09002114
Sequence 3, Application US/09002114
Setent No. 62/4720
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HOMAN PREPRONEUROTENSIN/NEUROMEDIN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.6%; Score 32; DB 5; Length 609; 50.0%; Pred. No. 3.1e+02;
                                                                                                                                     APPLICANT: AMGEN INC.

TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.

ZIP: 9132-1789

ZIP: 9132-1789

COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,114
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                 Sequence 4, Application PC/TUS9504075 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 609 amino acids
amino acid
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Best Local Similarity 50.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto STATE: CA
96 EELCHEKE 103
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96 EELCHEKE 103
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ZIP: 94304
                                                             RESULT 11
PCT-US95-04075-4
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08222619
Patent No. 5652352
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.

ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
TTY: Thousand Oaks
STATE: California
                             FILING DATE: 21-JULY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06727/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                   APPLICATION NUMBER: 08/505,012
                                                                                                                                                                                                   TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FUGTH: 609 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               69.68;
50.08;
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00996-5
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MOLECULE TYPE: protein
US-08-222-619-4
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|||:|:
77 EELCHEKE 84
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US-08-222-619-4
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Gaps

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Gaps
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50.0%; Pred. No. 2.1e+02;
tive 3; Mismatches 1; Indels
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ORGANISM: hazel (Corylus sp.)
IMMEDIATE SOURCE:
LIBRARY: POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
LENGTH: 160 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: hazel (Corylus Sp.)
IMMEDIATE SOURCE:
LIBRARY: POLLEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
US-07-847-010-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Breiteneder, Heimo
APPLICANT: Reikerstorfer, Arnold
APPLICANT: Valenta, Rudolf
APPLICANT: Valenta, Rudolf
APPLICANT: Walenta, Rudolf
APPLICANT: Breitenbach, Michael
APPLICANT: Rraft, Dietrich
APPLICANT: Rumpold, Heimut
APPLICANT: Scheiner, Otto
APPLICANT: Ebers, Fatima
TITLE OF INVENTION: Allergens of Alder Pollen and
TITLE OF INVENTION: Applications Thereof
NUMBES OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC COMPAtible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,010
FILING DATE: 01-JUN-1992
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: Jones III, Harry C
REGISTRATION NUMBER: 20,280
REFRENCE/DOCKET NUMBER: 6530-010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/07847010 Patent No. 5693495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 160 amino acids TYPE: amino acid
                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 50.00
نامح 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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97 EKVCHELK 104
                                                                                                                                                                                                                                                                                                                                           1 OKLCHOKK 8
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US-07-847-010-17
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57.1%; Pred. No. 1.5e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Breiteneder, Heimo
APPLICANT: Reikerstorfer, Arnold
APPLICANT: Reikerstorfer, Arnold
APPLICANT: Valenta, Rudolf
APPLICANT: Wolenta, Rudolf
APPLICANT: Breitenbach, Michael
APPLICANT: Breitenbach, Michael
APPLICANT: Rraft, Dietrich
APPLICANT: Rumpold, Helmut
APPLICANT: Scheiner, Otto
APPLICANT: Scheiner, Otto
APPLICANT: Ebner, Christof
APPLICANT: Farima
TITLE OF INVENTION: Applications Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,010
FILING DATE: 01-JUN-1992
CLASSIFICATION: 435
                     ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0450 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6530-010
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Patent No. 5693495
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONES III, HARTY C
REGISTRATION NUMBER: 20,280
REFERENCE/POCKET NUMBER: 6530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 169 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.4
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: GenBank
; CLONE: 163424
US-09-002-114-3
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STATE:
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                                                                 Length 160;
                                                                                                                                                                                                                                                                                                                         65.2%; Score 30; DB 1; Length 457; 66.7%; Pred. No. 5.1e+02; Live 2; Mismatches 0; Indels
           Query Match 65.2%; Score 30; DB 1; Length 160 Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 4; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         Query Match 65.2
Best Local Similarity 66.7
Matches 4; Conservative
                                           : |:||: |
97 EKVCHELK 104
                                     1 OKLCHOKK 8
                                                                                                                                                                                                                                                                                                                                                   1 QKLCHQ 6
US-07-847-010-17
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Search completed: November 1, 2002, 14:51:58 Job time: 1.66881 secs

1:111: 262 QRECHE 267

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(without alignments)
489.985 Million cell updates/sec
                                                                                                                             November 1, 2002, 14:40:53; Search time 1.8135 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                US-09-606-129A-19
46
1 QKLCHQKK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                       Perfect score:
Sequence:
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A_Geneseq_032802:* Database :

1. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4. /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
5. /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
6. /SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
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13. /SIDSI/gcgdata/geneseqy-embl/AA1991.DAT:*
14. /SIDSI/gcgdata/geneseqy-embl/AA1991.DAT:*
15. /SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1991.DAT:*
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21. /SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:*
22. /SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:*
23. /SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000 DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human secreted pro Novel human diagno Mouse CGICE protei Human immune/haema Human polypeptide Human protein sequ Human protein sequ Plasmodium falcipa Human prostate can Human colon cancer Human 23 kD basic Description SUMMARIES AAG76544 AAO12476 AAB95513 AAB93045 AAB18183 ABG07163 AAY29955 AAM84701 ABB12078 **AAB**75580 AAB56915 ΩI Query Match Length DB 76.1 73.9 73.9 73.9 73.9 Score 4 5 7 7 8 8 9 11 11 Result . 02

Human immune/haema		Human phosphatidic	Novel human diagno	Arabidopsis thalla	Novel human diagno	Novel human diagno	dopsis	human			Haematopoietic ste	Wild-type yeast tr	Loss-of-function m		Loss-of-function m	Loss-of-function m	Loss-of-function m	٠	Loss-of-function m	Loss-of-function m	Loss-of-function m	Human brain expres		Peptide #9876 enco		Human brain expres	Human bone marrow	Peptide #10214 enc	Human nervous syst	Human polypeptide	Peptide #1610 enco	Peptide #1633 enco	Protein #1567 enco
AAM87820	9	AAG78167	ABG22874	AAG08675		ABG11715	AAG08674	ABG20204	ABG27718	AAM25801	AAY79180	AAW79501	AAW79502	AAW79503	AAW79504	AAW79505	AAW79506	AAW79507	AAW79508	AAW79509	AAW79510	AAM59485	AAM72049	ABB42370	ABB25845	AAM63258	AAM76070	AAM36177	ABB16899	AA006457	ABB28959	ABB34127	ABB19568
22	22	22	22	21	22	22	21	22	22	22	21	19	19	13	19	19	19	19	19	19	19	22	22	22	22	22	22	22	22	22	22	22	22
51	87	112	196	197	210	220	242	305	435	678	778	23	23	23	23	23	23	23	23	23	23	33	33	52	55	55	52	52	99	87	88	88	88
71.7	71.7	71.7	71.7	71.7	71.7		71.7		ij	71.7	Ξ.	9.69	6	٩.	9.69	6	6	6	9.	6	6	9.69	9.	6	9.	9.	9.		δ.	6	9.69		φ.
33	33				33										32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ABB12078 standard; peptide; 141 AA ABB12078; RESULT 1 ABB12078

ALIGNMENTS

Human 23 kD basic protein homologue, SEQ ID NO: 2448.

11-JAN-2002 (first entry)

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; haematopoiesis chemokinesis; thrombolysis, oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antlinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.

J5-FEB-2001; 2001WO-US03800. WO200157188-A2. Homo sapiens.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

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WO200077026-A1.
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                                                                                                                            food additive.
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                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                11-JUN-1999;
                                                                                                                                                                                                                                                              21-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
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Matches
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δλ
                                                                                                                                                                                                                                                                                                                conditions, equiences ABAN0925-ABAN0954 represent nucleic acids encoding them. The lawention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the movel polypeptides, and percent of the invention, methods of producing the navel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of the invention. Although novel, many of the bill of polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activities; and hence correctly activity; itssue growth activity; contractly activity; activity; tissue growth activities; confinentation activities; themostatic thrombolytic activities; themostatic, thrombolytic activities; activities; hemostatic, thrombolytic activities; activities; hemostatic, thrombolytic activities; activities; paemostatic, thrombolytic activities; and activities; concer cell proliferation or metastasis.

Conditions, e.g., by protein or ligand activities; or may be invention are useful for preventing, treating or amplicating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or preventing, treating or amplicating disease, are useful for preventing, treating or amplicating disease, are useful for preventing, the immunoactic conditions activities may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used in cell cultures to surnate by an encoder to meuraphy and the reample, such polypeptides may be used in the treatment of viral, and the and tungal infections in addition to immune disorders.

Compute part cell growth factor activity may be used to neuroper per per cell surnary and prov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                    Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein sequence encoded by gene 28 SEQ ID NO:134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that can be used to augment or replace cells damaged by illness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 22; Length 141;
Pred. No. 20;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Claim 20; Page 305; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75580 standard; Protein; 91 AA.
                                                               Drmanac RT;
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                                                                                                        WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AA;
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                                                               Liu C,
                                                                                                                               N-PSDB; ABA09322
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                                                             Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75580;
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Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide sequences AAF64176 - AAF6424. The specification includes amino acid sequences AAB75555 - AAB75066 which represent fragments of the human secreted proteins, and protein sequences with which they share homology. The proteins and polynucleotides, their agonists and antagonists have activities dependent on the tissues and cells in which they are expressed, examples of these activities include, immunosuppressive; antiarthritic antirheumatic; antiproliferative; cytostatic; cardiant; and sactivities include; immunosuppressive; correspondentive; notropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; and vulnerary. The proteins, colynucleotides, agonists and antagonists can be used to treat or detect or diagnose various diseases and disorders including, autofimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders of e.g. cardiac arthritis, hyperproliferative disorders arthritis and all and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
antiproliferative, cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; cardiovascular disorder; hyperproliferative disorders; cerebrovascular disorder; wound healing; nervous system disorder; ocular disorder; skin ageing; chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which are used in the isolation, identification and characterisation of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2000; 2000WO-US14973.
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA;
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m

us-09-606-129a-19.rag

ABG07163;

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The present sequence represents the mouse CGICE protein. When the CGICE gene is mutated it is responsible for Best's macular dystrophy (BMD). Polynucleotides encoding CGICE are useful for dagnosating whether a patient carries a mutation in the CGICE gene. Normal and mutated CGICE proteins are useful for identifying activators and/or inhibitors of these proteins, in order to treat BMD. The CGICE gene offers a simpler and cheaper method of diagnosing BMD without the need for the presence of the patient. The gene may also be useful to discovering the genetic cause of age-related macular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                  CGICE; Best's macular dystrophy; mutation; diagnosis; detection;
BMD; age-related macular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human and mouse polynucleotides encoding CGICE polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 20; Length 551;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:12294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wadelius C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metzker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM84701 standard; Protein; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 8; 67pp; English.
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62.5%;
                                                           Mouse CGICE protein sequence.
                                                                                                                                                                                                                                                                                                                          98US-0075941.
                                                                                                                                                                                                                                                                                   09WO-US03790
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                   22-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petrukhin K, Caskey CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC (UYUP-) UNIV UPPSALA.
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N-PSDB; AAZ21229.
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490 QEICHMKK 497
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                                                                                                                                                                                                                                                                                                                          25-FEB-1998;
18-DEC-1998;
                                                                                                                                                                                                                                                                                   22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM84701;
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                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeratase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful in medical clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasorders for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand on acid sequences. ABG0010-ABG30377 represent novel human cald sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo int/pub/published_pct_sequences.
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                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 37522; 103pp; English.
                                                                                                Novel human diagnostic protein #7154.
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ilarity 62.5%;
Conservative
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Best Local Similarity
Thes 5; Conserva
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134 EKLCHSRK 141
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1; Indels

Seguence

AAY29955

AAY29955 ID AAY2 XX AC AAY2 RESULT 4

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2000US-0237037

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1.Jan-2000 4-FEB-2000 2-MAR-2000 5-MAR-2000 7-MAR-2000 9-MAY-2000 9-MAY-2000 9-JUN-2000 0-JUN-2000 0-JUN-2000 1-JUL-2000 1-JUL-2000 1-JUL-2000 1-JUL-2000	14 - AUG - 2000 14 - AUG - 2000 15 - AUG - 2000 16 - AUG - 2000 17 - AUG - 2000 18 - AUG - 2000 19 - AUG - 2000 10 - SEP - 2000 10 - S	8 SEP - 2000 2 SEP - 2000 2 SEP - 2000 4 SEP - 2000 4 SEP - 2000 4 SEP - 2000 6 SEP - 2000 7 SEP - 2000 6 SEP - 2000
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2000US-0237038 2000US-0237039 2000US-0239935 2000US-0241291 2000US-0241281 2000US-0241186 2000US-0241186 2000US-0241186 2000US-0241806 2000US-0241806 2000US-0246477 2000US-0246477 2000US-0246527 2000US-0246527 2000US-0246528 2000US-0249209 2000US-0249209 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-0249218 2000US-024928 20000S-0256719 20000S-0251479 20000S-0251865 20000S-0251868 20000S-0251869 20000S-0251869 20000S-0251990 20000S-0251990 02-OCT-2000; 2 02-OCT-2000; 2 02-OCT-2000; 2 02-OCT-2000; 2 13-OCT-2000; 2 13-OCT-2000; 2 20-OCT-2000; 2 20-OCT PRANT SERVICE SERVICE

SM; Ruben (HUMA-) HUMAN GENOME SCI INC Barash SC, Rosen CA,

WPI; 2001-483426/52. N-PSDB; AAK57482.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

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88 AA;
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62 QELCHQQE 69
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03-NOV-1999;
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                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG76544;
                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                        AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
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                                 Claim 11; SEQ ID NO 12294; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer antigen protein sequence SEQ ID NO:1493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 22; Length 60;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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wound; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.98;
71.48;
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Matches 5; Conservative
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N-PSDB; AAF16118.
                                                                                                                                                                                                                                                                                                                                                                                                               60 AA;
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47 RLCHKKK 53
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metastasis
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AAB56915
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                         proteins, called prostate cancer antigens, given in AAB5363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P.
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AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colon cancer; colon cancer antigen; diagnosis; detection;
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Pred. No. 65;
3; Mismatches
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62.5%;
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99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal carcinoma
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Best Local Similarity
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at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                 AAB95513;
                             Seguence
                                                     Query Match
                                                                             Matches
                                                                                                                                                                             AAB95513
                                                                   Best
                                                                                                                                                                  RESULT
     SXX
                                                                                                      δ
                                                                                                                            Dp
                                                                                                                                                                                                     0
Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell co express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA01910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchie; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                    missing at time of publication, meaning no sequence listing were SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                DB 22; Length 102; 74;
                                                                                                                                                                             Indels
                                                                                                                                                                             ;
0
                                                               present invention.
N.B. Pages 666 to 682 and page 7053 of the
                                                                                                                                                                 Pred. No. 74; ; Mismatches
                                                                                                                                                      Score 34;
                                                                                                                                                                                                                                                                                         AAO12476 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 26368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT;
                                                                                                                                                    73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                  Query Match 73.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-514838/56.
                                                                                                                            102 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI92407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200164835-A2.
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61 ICHQKK 66
                                                                                                                                                                                                    3 ІСНОКК В
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                 AA012476;
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                  RESULT 8
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The present invention describes primer sets for synthesising 5602

[ull-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence, where the
coligonucleotide which comprises at least 15 nucleotides and the compination of
the 5'-end sequence, 3'-end sequence 15'-end 16'-end 16'-e
                                                                                                                                                                                 ö
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                                                                                                                                                                                 Gaps
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                                                                                   Length 104;
                                                                                                                                                                                 1; Indels
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki
                                                                                        Score 34; DB 22;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 18081; 2537pp + CD ROM; English.
                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:18081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB95513 standard; Protein; 522 AA.
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                        73.9%;
71.4%;
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                                                                                                                                                                                 Conservative
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                                                                                                                                  Local Similarity
nes 5; Conserv
104 AA;
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                                                                                                                                                                                                                                                                                                                                                        60 RFCHOKK 66
                                                                                                                                                                                                                                                                     2 KLCHQKK 8
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11-JAN-2000;
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or .0) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to opplynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence.
represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs of
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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0
                                                                                               Length 522;
                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K,
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 11834; 2537pp + CD ROM; English.
                                                                                         Score 34; DB 22;
Pred. No. 3.2e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:11834.
                                                                                                                                                                                                                                                                                                                AAB93045 standard; Protein; 790 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                           73.98;
62.58;
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                           Query Match 73.9
Best Local Similarity 62.5
Matches 5; Conservative
                    of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
                                                         522 AA;
                                                                                                                                                                                                                157 QELCHQQE 164
                                                                                                                                                                         1 ОКІСНОКК 8
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                                                                                                                                                                                                                                                                                                                                                       AAB93045;
                                                           Seguence
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) and the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic biology, a process hampered by the complexity of the parasitic biology, a process hampered by the resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not
                                                                                                                                                   ö
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum chromosome 2 related protein SEQ ID NO:40.
                                                                                                                                                   ö
                                                                                                            Length 790;
                                                                                                                                                   0; Indels
                                                                                                            Score 34; DB 22;
Pred. No. 4.7e+02;
3; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 101-104; 577pp; English.
                                                                                                                                                                                                                                                                                                                          AAB18183 standard; Protein; 1188 AA.
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                                                                                                              73.9%;
62.5%;
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                                                                                          Query Match
Best Local Similarity 64...
5. Conservative
                                     of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365347/31.
                                                                          790 AA;
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157 QELCHQOE 164
                                                                                                                                                                                       1 QKLCHQKK 8
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                                                                            Sequence
                                                                                                                                                                                                                                                                                   RESULT 11
AAB18183
 SSSSXS
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01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229509.
06-SEP-2000; 2000US-0229509.
06-SEP-2000; 2000US-0229509.
06-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0230438.
08-SEP-2000; 2000US-0231242.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-02314113.
08-SEP-2000; 2000US-02314113.
08-SEP-2000; 2000US-0231988.
14-SEP-2000; 2000US-023399.
15-SEP-2000; 2000US-023399.
16-SEP-2000; 2000US-023399.
17-SEP-2000; 2000US-023399.
18-SEP-2000; 2000US-023399.
18-SEP-2000; 2000US-023399.
19-SEP-2000; 2000
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                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                        Gaps
                                                                                                      ;
                                                               Score 34; DB 21; Length 1188; Pred. No. 6.8e+02; 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen SEQ ID NO:15413.
   specifically mentioned within the specification
                                                                                                                                                                                                                                                   AAM87820 standard; Protein; 51 AA
                                                                  Ouery Match 73.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative 2
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2000US-021647
2000US-0216807
2000US-0216807
2000US-021487
2000US-0228290
2000US-0224518
2000US-0224518
2000US-0225213
2000US-0225214
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                                     1188 AA;
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1117 EELCHQK 1123
                                                                                                                                    1 QKLCHQK 7
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                                     Seguence
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                              Human immune/haematopoietic antigen SEQ ID NO:11225
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07-NOV-2001 (first entry)
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23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                 16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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11-JUL-2000;
11-JUL-2000;
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22-AUG-2000;
22-AUG-2000;
                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                             07-JUN-2000;
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14-AUG-2000;
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01-SEP-2000;
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   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
csupplement the patients own production of (I). Additionally, (I)
concletion and polynucleotides may be used to protect the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
co AAK87694 represent inwention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and mersetasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM83632 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
                                                                                                                                                          2000US-0250160.
2000US-0250391.
2000US-0251030.
2000US-0251988.
                                                                                                                                                                                                                                                  2000US-0251856.
2000US-0251868.
2000US-0251869.
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                                                                                                                              2000US-0249299.
2000US-0249300.
                                                       2000US-0249244
                                                                    2000US-0249245
2000US-0249264
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2000US-0251990,
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Matches 5; Conservative
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N-PSDB; AAK60601.
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                       17 - NOV - 2000;
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01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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RESULT 13 AAM83632

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2000US-0249216.
2000US-0249217.
2000US-0249218.
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                                       2000US-0235834
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                                                 29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
               21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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13-0CT-2000;
13-0CT-2000;
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08-NOV-2000;
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20-OCT-2000;
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08-NOV-2000;
08-NOV-2000;
                                       27-SEP-2000;
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02-OCT-2000;
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02-OCT-2000;
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08-NOV-2000;
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17-NOV-2000;
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amino acid sequences given in AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting the nection and polynucleotides may be used to produce the secreted (I), by inserting concers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hamatopoietic antigen genomic sequences from the present invention. AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention.
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0
                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis ,
                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
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immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
human immunodeficiency virus; HIV; infection; immunological disease;
                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 11225; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 33; DB 22; Length 87; 71.4%; Pred. No. 96; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human phosphatidic acid phosphatase 2-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG78167 standard; Protein; 112 AA
                                                                                                                                          Ruben SM;
                                                                                                      (HUMA-) HUMAN GENOME SCI INC
              08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                          Rosen CA, Barash SC,
                                                                                                                                                                           WPI; 2001-483426/52.
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76 QLCHKKK 82
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Search completed: November 1, 2002, 14:47:08 Job time : 3.8135 secs
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                                                                                                                                                                                             with cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic activity. The protein and encoding polynucleotide are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The polynucleotide is useful in gene therapy.
                                                                                      Human phosphatidic acid phosphatase 2-12 and encoded polynucleotide, used in diagnosis and treatment of malignant tumours, haemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                 The invention relates to the human phosphatidic acid phosphatase 2-12
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                   Score 33; DB 22; Length 112;
Pred. No. 1.2e+02;
4; Mismatches 0; Indels
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(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #22865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG22874 standard; Protein; 196 AA.
                                                                                                                                                         Claim 1; Page 31; 35pp; Chinese.
                                                                                                                                                                                                                                                                                                    71.78;
50.08;
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                                                                                                                                                                                                                                                                                                                              Conservative
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N-PSDB; AAS87061.
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                                                 WPI; 2001-597124/67
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          Sequence 112 AA;
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                                                              N-PSDB; AAI64606
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                                                                                                                                inflammation
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                       мао У,
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in the subject of (II) and (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human can appear in the printed specification, but was obtained in electronic format directly from WIPO
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83.3%;
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Best Local Similarity
Matches. 5; Conserv
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RESULT 1
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                                                                  November 1, 2002, 14:43:08; Search time 1.2717 Seconds (without alignments) 952.238 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                             OM protein - protein search, using sw model
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Q9BRW8
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Q9DD21
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049511
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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Maximum DB seq length: 2000000000
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09P0U6 043658 04HD98 09HD98 09HD99 090532 09UL13 09UL13 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL14 09UL18 09UL19 00SUL19 00SU	0 00
44444644814481444141	87H2H
0.000000000000000000000000000000000000	80.0 80.0 80.0 77.5
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11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4444

#### ALIGNMENTS

DOCK64  DOCK64  DOSCK64  DO 09CX64  DT 01-JUN-2001 (TrEMBLrel. 17, 05 00001N03RIK PROTEIN. 2500001N03RIK PROTEIN. OS MUS musculus (Mouse).  CENKATYOCA: MetaZoa; Chordata OX NUBL TAXID=10090;  RP SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RA MEDLINE-21085660; Pubmed=112 RA ALARWA T., HARA A., SANDI RA ALARWA K., MATSUDA H.A., ASH RA SALOT T., OKAZAKI Y., FURUNO MRA SALOT Y., OKAZOT S., MATSUO Y. SCHRIMI L.M., STAUDII F., SONTIMI L.M., STAUDII F., SONTIMI L., MAS NORGONE P., BOTTONI D., BOTTONI RA BLOWNSTEIN M.J., BUIT C., FI RA LONDS P., MATCHIDONI D., BOTTONI RA SASAKI H., SACO K., SCHOEDDA SAZAKI Y., SACO K., SCHOEDDA SA SAZAKI Y., SACO K., SCHOEDDA SA SAZAKI Y., SACO K., SCHOEDDA SACO SACO SACO SACO SACO SACO SACO SAC	14.1  999YEA  999YEA  999YEA  999YEA  999YEA  999YEA  901-JUN-2001 (TrEMBLrel. 17, Last sequenc  901-JUN-2001 (TrEMBLrel. 17, Schurognat  901-JUN-2001 (TREMBLRel. 17, Mashima J., Mazhinchione)  901-JUN-2001 (TREMBLRel. 17, Schoenbach C., Seya  901-JUN-200-Seya  901-JUN-200 (TREL. 18, Schoenbach C., Seya  901-JUN-200 (TREL. 18	PRT; , Created) , Last sequence anno last anno	14.1  1992Y64  1993Y64  101-JUN-2001 (TrEMBLrel. 17, Last sequence update)  101-JUN-2001 (TrEMBLrel. 17, Last sequence update)  101-JUN-2001 (TrEMBLrel. 17, Last sequence update)  101-JUN-2001 (TrEMBLrel. 17, Last annotation update)  101-JUN-2001 (TrEMBLrel. 17, Last annotation update)  101-JUN-2001 (TrEMBLrel. 17, Last annotation update)  102500001N03RIX  102500001N03RIX  10250001N03RIX  10350001N03RIX  10350000N0N  10350000N  1035000N  103500N  103500N  103500N  103500N  103500N  103500N  103500N  103500N
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MGD; MGI:1917355; 2500001N03Rik.

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Q9XZM5 Q9H007 Q9UIJ2

Q9BRW8 Q9BRW8

RESULT 2

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Matches

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN-C575BL/65; TISSUB-KIDNEY;

MEDLINE-2108566; PubMed-11217851;

A rakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Asato T., Osazaki Y., Gojobori T., Bono H., Banalov S., Casawant T.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Barke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Barke J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

M. Winner, Pall M., Wang K.H., Weitz C., Whittaker C., Wilming D.,

M. Winner, Pall M., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A. Winner, Pall M., Wang K., Wang K., Kawaji H., Kohtsuki S.,

A. Winner, Pall M., Wang K., Wang K., Wawaji H., Kohtsuki S.,

A. Winner, Pall M., Wang K., Wang W., Kawaji H., Kohtsuki S.,

A. Winner, Pall M., Wang W., Kawaji H., Kohtsuki S.,
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu S.X., Chan A., Yu G., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H., Toriumi M., Chung M., Goldsmith A., Liu A., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao O., Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 11; Length 303; 100.0%; Pred. No. 1; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52D8A3B02EE956EB CRC64;
                                                                                                           Last sequence update)
Last annotation update)
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                                                                                      Created)
                                              PRT;
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Pfam; PF01408; GFO_IDH_MOCA; 1.
SEQUENCE 303 AA; 34491 MW; 52DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK002231; BAB21950.1; -.
MGD; MGI:1915580; 0610006A11Rik.
                                                                                                        (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                    01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001
                                                                                                                                                   0610006A11RIK PROTEIN.
                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F10K1.11 PROTEIN.
                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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274 KKRILHC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKRILHC 7
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                                                                                                             01-JUN-2001
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                                                                  Q9DD21;
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                                              Q9DD21
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Q9LML0
                        Q9DD21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
NCBL_maxID-9666;
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0
                                                                                    Score 40; DB 11; Length 295;
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                                                                                                                                 Indels
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Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC008455; AAH00456.1; -
SEQUENCE 296 AA; 33428 MW; 2CF2AA7F1CDDB707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005902; AAH05902.1; -InterPro; IPR000683; GFO_IDH_MocA.
                 Pfam; PF01408; GFO_IDH_MOCA; 1.
SEQUENCE 295 AA; 33524 MW; F2E1682ED77032A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33432 MW; A389AFDDB6ADBABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:14706).
                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                            0; Mismatches
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0; Mismatches
                                                                                                        Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR000683; GFO_IDH_MocA.
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                                                                                    100.08;
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                                                                                                                                 Conservative
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Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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274 KKRILHC 280
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275 KKRILHC 281
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275 KKRILHC 281
                                                                                                                                                                       1 KKRILHC 7
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RESULT 3 Q96QL4

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Submitted (FEB-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.
Bancroft I., Mewes H.W., Mayer K., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F28J12.70 OR Ar4G18410.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Ecker J.R., Federspiel N.A., Theologis A.; "The sequence of BAC F10K1 from Arabidopsis thaliana chromosome 1."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 Gaps
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Last annotation update)
LIKE PROTEIN (MUDR TRANSPOSABLE ELEMENT-
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                                                                                                                                                                                                       Length 512;
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                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                       EMBL; AC06ACTOR: FAD (BY SIMILARITY).

EMBL; AC067971; AAF82202.1; -
Interpro; IPR001327; FAD_pyr_redox.

Pfam; PF00070; pyr_redox!

FAD; Flavoprotein; Oxidoreductase.

SEQUENCE 512 AA; 56857 WW; 1F63AFA9A1A2C13B CRC64;
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EMBL; AB017068; BAB11366.1; -.
SEQUENCE 599 AA; 69407 MW; 36BAEE2F2A82D717 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9FHV3;
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                   Score 38; DB 10;
Pred. No. 4.4;
1; Mismatches 0;
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Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-COLUMBIA;
MEDLINE-99397451; PubMed-10470850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUDE TRANSPOSABLE ELEMENT - 19, LIKE PROTEIN).
                                                                                                                                                                                                         95.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         049511:
01-JUN-1998 (TrEMBLrel: 06,
01-JUN-1998 (TrEMBLrel: 06,
01-DEC-2001 (TrEMBLrel: 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative.
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 KKRLLHC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                      1 KKRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KKRILHC 7
                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FHV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                 09FHV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       049511
                                                                                                                                                                                                                                                                                                                            Q
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A TUMOR SUPPRESSOR.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 2 ISOPORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: IN THE ADULT, WIDELY EXPRESSED WITH HIGHEST

LEVELS IN THYMUS AND TESTIS. EXPRESSED THROUGHOUT THE WHOLE EMBRYO
AT ALL STAGES OF DEVELOPMENT EXAMINED. AT DAY 10, HIGHEST

EXPRESSION IS FOUND IN THE YOLK SAC WHILE AT DAY 16 AND 18, HIGHER

LEVELS ARE FOUND IN INDER COMPARTMENTS OF BONE.

-!- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OF ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN-129/SVJ; TISSUE-BRAIN, EMBRYONIC FIBROBLAST, AND SPLEEN;
MFDLINE-20011419; Pubmed-10542254;
Zeremski M., Hill J.E., Kwek S.S.S., Grigorian I.A., Gurova K.V.,
Garkavtsev I.V., Diatchenko L., Koonin E.V., Gudkov A.V.;
"Structure and regulation of the mouse ingl gene. Three alternative
transcripts encode two PHD finger proteins that have opposite effects
on p53 function."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: ISOFORM I INHIBITS P53-DEPENDENT TRANSCRIPTIONAL ACTIVATION AND MAY FUNCTION AS AN ONCOPPOTEIN. ISOFORM 2 ACTS AS NEGATIVE GROWTH REGULATOR BY COOPERATING WITH P53 IN TRANSCRIPTIONAL ACTIVATION OF P53-RESPONSIVE GENES AND MAY ACT AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rancourt D., Garkavtsev I.;
"Structural organization and expression pattern of the murine ING1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 38; DB 10; Length 633; 85.7%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21710; CAA16721.1; -.
EMBL; AL161548; CAB78843.1; -.
                                                                                         Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72930 MW; 3FC298BF2218C623 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         090xv3; 090xv4; 090UPB; 0902x3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on p53 function.";
J. Biol. Chem. 274:32172-32181(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004332; MuDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03108; MuDR;
SEQUENCE 633 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KKRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ING1 PROTEIN.
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1 KKRILHC 7
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                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09ST63;
                                                                                                                                                                                                                                                                                                                                                               Q9AKSO;
                                                                                                                                                                                                                                                                                                                                        Q9AKS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ST63
                                                                                                                                                                                                                                                                                         RESULT 10
Q9AKS0
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                 Best
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  DR
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=TONGUE;

XX MEDINE=21085660; DubMed=11217851;

X MADLINE=21085660; DubMed=11217851;

X Arawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

X Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kandota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Achim L. M., Gaasterland T., Gissi C., King B., Kochiwa H.,

X Schrim L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Kuons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N.,

Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyanshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyanshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
1 IS FOUND AT DAY 11 WHILE HIGHEST EXPRESSION OF ISOFORM 2 IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM 2).
L -> F (IN REF. 2).
6765C984EEF179F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2'-5' OLIGOADENYLATE SYNTHETASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                         Oncogene; Anti-oncogene; Alternative splicing. DOMAIN 210 259 PHD-FINGER.
                                    -1- SIMILARITY: CONTAINS 1 PHD-FINGER DOMAIN.
EMBL; AF17755; AAF16911.1; -.
EMBL; AF17755; AAF16908.1; -.
EMBL; AF177575; AAF16910.1; -.
EMBL; AF19820; AAF16910.1; -.
EMBL; AF19820; AAF16910.1; -.
EMBL; AF19820; AAF16910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1
Pred. No. 6.8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001797; 25A_synth.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR00626; Ubiquitin.
SMART; SM00213; UBQ; 1.
PROSITE; PS00833; 25A_SYNTH_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                               32109 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                      PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                  SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                               MGD; MGI:1349481; Ingl
InterPro; IPR001965; P
                                                                                                                                                                                                                                           Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                               279 AA;
                  FOUND AT DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|:|||
67 KRRVLHC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D6S2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D6S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplanae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heikkilae M.P., Honisch U., Wunsch P., Zumft W.G.;
"Role of the Tat transport system in nitrous oxide reductase
translocation and cytochrome cdl biosyntheis in Pseudomonas
                                                                                                   Score 36; DB 11; Length 508;
Pred. No. 12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 2; Length 267;
Pred. No. 11;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE INTERNAL ROTENONE-INSENSITIVE NADH DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liducari...,
stutzeri...,
J. Bacteriol. 183:1663-1671(2001).
EMBL; AJ299712; CAC29149 1; -
InterPro; IPR002033; UPF0032.
Pfam; PF00902; UPF0032; 1.
PROSITE; PS01218; UPF0032; 1.
PROSITE; PS01218; UPF0032; 1.
PROSITE; PS50152; 25A_SYNTH_3; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
SEQUENCE 508 AA; 58767 MW; 9552B4540CC801A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. DESIREE; TISSUE-LEAF;
MEDLINE-20040052; Pubmed=10571867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21101859; PubMed=11160097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%;
71.4%;
                                                                                                         90.08;
                                                                                                                                71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Plant J. 20:79-87(1999)
                                                                                                                                Local Similarity
                                                                                                                                                                                                                                          |||::||
109 KKRLIHC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4113;
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21 RKRLLHC 27
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                                                                                                                                                                                                             1 KKRILHC 7
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Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ING1 ISOFORM (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania amazonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOMAL PROTEIN L44.
                                                                  SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                    Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein
                                                                                                                                                                                                                                                                                                        236 KRRLLHC 242
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6 KKKVMHC 12
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                              thaliana
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MEDLINE-20083487; Pubmed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:B1088C09.";
                                                                                            / Match 87.5%; Score 35; DB 10; Length 495; Local Similarity 71.4%; Pred. No. 19; onservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%; Score 35; DB 10; Length 499; 71.4%; Pred. No. 19; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AP003734; BAB68119.1; -.
SEQUENCE 499 Aa; 54687 MW; AF4337AB3F9363D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE NADH DEHYDROGENASE (UBIQUINONE OXIDOREDUCTASE).
           EMBL; AJ245861; CAB52796.1; -...
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00070; pyr_redox; 1...
FAD; Flavoprotein; NAD; Oxidoreductase.
SEQUENCE 495 AA; 54902 MW; 6AFFC807BEB01340 CRC64;
                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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 -! - COFACTOR: FAD (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
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                                                                                                                                                                  1:1:111
224 KRRLLHC 230
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                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4530;
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                                                                                                                                                 1 KKRILHC 7
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Matches
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Gaps
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NCBL_TaxID=5659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porter-Kelley J., Chaudhuri G.;
"Cloning and characterization of Leishmania ribosomal protein L44."
"Cloning and characterization of Leishmania ribosomal protein L44."
"Lamilted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-1 - SIMILARITY: BELONGS TO THE L44E FAMILY OF RIBOSOMAL PROTEINS.
EMBL, AF148853; AAD31928.2; --
InterPro. IPRO0552; Ribosomal_L44E.
Pfam; PF00935; Ribosomal_L444: 1.
PROSITE; PS01172; RIBOSOMAL_L44E; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhinl; Hominidae; Homo.
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0
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                                                                                                                                                                                                                      87.5%; Score 35; DB 10; Length 508; ilarity 71.4%; Pred. No. 19; Conservative 2; Mismatches 0; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                     -:- COFACTOR: FAD (BY SIMILARITY).

EMBL; AC004680; AAC31853.1; -:
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00070; pyr_redox: 1...
FAD; Flavoprotein; Oxidoreductase; Ubiquinone.
SEQUENCE 508 AA; 56503 MW; 266A434E702A0C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 AA; 12283 MW; F30A3AB2047B0334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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Wed Nov 6 14:28:02 2002
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OX NCBL_TaxID=9606;
RN | 1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20322670; PubMed=10866301;
RA Mehmet G., Ouchida M., Fukushima K., Hanafusa H., Etani T.,
RA Mehmet G., Ouchida M., Fukushima K., Hanafusa H., Etani T.,
RA Mishioka S., Nishizaki K., Shimizu K.;
RT "Genomic Structure of the Human Incl Gene and Tumor-specific Mutations
RT Gencer Res. 60:1343-3146(2000).
RE EMBL; AB037594; BAB20992.1; -.
RE EMBL; AB037594; BAB20992.1; -.
RE NON_TER 111 111
SQ SEQUENCE 111 AA; 12566 MW; 9C76D21C7E982313 CRC64;
Guery Match
Ratches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps O;
CONSERMINEC 56
Search completed: November 1, 2002, 14:49:50
Job time: 2.2717 secs
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:41:32; Search time 0.360129 Seconds (without alignments) 752.611 Million cell updates/sec Run on:

US-09-606-129A-34 40 1 KKRILHC 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

No.	Description	٠	P53004 homo sapien		Q9z2f2 mus musculu	Q92630 homo sapien			P40020 saccharomyc	mus m	P26885 homo sapien	sacch	P55326 caenorhabdi					_	-				P51956 homo sapien		emeri	_	P20370 acinetobact		P96172 vibrio sp.	033525 rhizobium l		P37179 escherichia	9432 rattu	4094 homo	11 11 2 1 m 2 2 2 2 0
SUMMARIES	ID		BIEA_HUMAN	BIEA_RAT	OASL_MOUSE	DYR2_HUMAN	AMP1_LYCES	AMPL_SOLTU	PIP1_YEAST	FKB2_MOUSE	FKB2_HUMAN	YHP5_YEAST	YZG1_CAEEL	SHP1_YEAST	SUN_HAEIN	YD2H_SCHPO	REP_HAEIN	CAPU_DROME	YZ09_METJA	YAT6_RHOBL	CYCH_XENLA	DGTP_MYCSM	NEK3_HUMAN	DYR3_HUMAN	SEPA_EMENI	PRKD_MOUSE	DC4C_ACICA	Y113_NPVAC	OTCA_VIBS2	MDH_RHILV	MDH_RHIME	HYBA_ECOLI	ODPB_RAT	CYCI_HUMAN	CYCL MOUSE
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	Length		736	295	473	528	571	573	925	140	141	144	257	423	451	260	670	1059	108	249	323	428	459	288	1790	4128	134	169	301	320	320	328	359	377	377
αÞ	Query Match		100.0	95.0	90.0	82.2	80.0	80.0	80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5
	Score	1	2	38	36	33	32	32	32	31	31	31	31	31	31	31	31	31	30	30	30	30	30	30	30	30	29	53	53	29	29	53	29	29	29
	Result No.		-	7	e	4	S	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	92	27	28	29	30	31	32	33

09x0x7 thermotoga P2552 escherichia P18140 tacaribe vi P43704 haemophilus 005542 gluconobact P55468 human herpe 064347 mus musculu P35524 rattus norv 047077 enterobacte 075643 homo sapien P79114 bos tautus 09hd67 homo sapien
PURZ THEMA GPPA_ECOLI NCAB_TACV TOP3_HAEIN DHET_GLUOX ULS2_HSV7J CLC1_MOUSE CLC1_RAT BGAL_EMYCL US2Q_HUMAN MY10_BOVIN
400 494 570 651 757 861 994 1028 1701 2052
722.5 722.5 722.5 722.5 722.5 722.5 722.5
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## ALIGNMENTS

RESOLUTION OF SEQUE RAY MADINE REAL SEQUE RAY MADINE RA
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PATHWAY: FINAL STEP IN HEME METABOLISM,
                           SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: TO E.COLI YHHX.
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274 KKRIMHC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKRILHC 7
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SEQUENCE
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MUTAGEN
MUTAGEN
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McCoubrey W.K. Jr., Maines M.D.;

"Site-directed mutagenesis of cysteine residues in biliverdin
reductase. Roles in substrate and cofactor binding.";

Eur. J. Biochem. 222:597-603(1994).

-! FUNCTION: CONVERTS BILIVERBIN TO BILIRUBIN: DISPLAYS TWO DISTINCT
PH OPTIMA USING A DIFFERENT COFACTOR AT EACH PH: NADH AT THE LOWER
PH 6.7-6.9 RANGE AND NADHP AT PH 8.5-8.7. NADPH, HOWEVER, IS THE
PROBABLE COFACTOR IN BIOLOGICAL SYSTEMS.
-! CATALYTIC ACTIVITY: Bilirubin + NAD(P)(+) = biliverdin + NAD(P)H.
-!- COFACTOR: BINDS ONE ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fakhrai H., Maines M.D.;
"Expression and characterization of a cDNA for rat kidney biliverdin
reductase. Evidence suggesting the liver and kidney enzymes are the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ODFD3B386F4DFC0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (POTENTIAL).
ZINC (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-VAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Biol. Chem. 267:4023-4029(1992).
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000683; GFO_IDH_MocA. Pfam; PF01408; GFO_IDH_MocA; 1. Oxidoreductase; NAD; NADP; Zinc.
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MEDLINE-92156147; Pubmed=1371282;
                                                                                                                                                                                                                                                                                                                   EMBL; AC005189; AAC25526.1; -. MIM; 109750; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33488 MW;
                                                                                                                                                                                                                                                          EMBL; X93086; CAA63635.1; -. EMBL; U34877; AAC35588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA;
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275 KKRILHC 281
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A Tiefenthaler M., Marksteiner R., Neyer S., Koch F., Hofer S.,

A Tiefenthaler M., Marksteiner R., Neyer S., Koch F., Hofer S.,

Schuler G., Nussenzweig M., Schneider R., Heufler C.;

MI204, a novel 2',5' oligoadenylate synthetase with a ubiquitin-like

extension, is induced during maturation of murine dendritic cells.";

L. Timunol. 163:760-765(1999).

C. I- FUNCTION. MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS

INPECTION, CONTROL OF CELL GROWNT, DIFFERENTIATION, AND APOPTOSIS.

C. I- CATALYTIC ACTIVITY: BINDS DOUBLE-STRANDED RNA AND POLYMERIZES ATP

INTO PPPR(A2'P5'A)N OLIGOMERS, WHICH ACTIVATE THE LATENT RNASE L.

THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAS.

C. I- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SPLEEN DENDRITIC CELLS,

WHEREAS, IN BONE MARROW-DERIVED DENDRITIC CELLS,

WHEREAS. IN BONE MARROW-DERIVED DENDRITIC CELLS,

THE HIGHEST LEVELS BEING IN THYMUS, LUNG, AND BONE MARROW.

C. I- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.

C. I- SIMILARITY: BELONGS THE TRUE ORTHOLOG OF HUMAN OASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q922F2;
16-CCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
54 kba 2'-5'-0ligoadenylate synthetase like protein (EC 2.7.7.-) (p54 OASL) (p54OASL) (M1204).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Score 38; DB 1; Length 295; 85.7%; Pred. No. 0.77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219C8EA96C150588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C->A: LOSS OF ACTIVITY.
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
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ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
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                                                                                                                                                                                                                                                        EMBL; M81681; AAA40830.1; -.
InterPro; IPR000683; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA.
Oxidoreductase; NAD; NADP; Zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33565 MW;
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Matches 6; Conservative
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295 AA;
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Becker W., Joost H.-G.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IN VITRO; CAN PHOSPHORYLATE HISTONES H3 AND H2B ON SER
- AND THR RESIDUES. WAY BE INVOLVED IN THE REGULATION OF CELLULAR
GROWTH AND/OR DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence characteristics, subcellular localization, and substrate specificity of DYRK-related kinases, a novel family of dual specificity protein kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC.
PTM: AUTHOPHOSPHORYLATED ON TYR RESIDUES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98421512; PubMed-9748265;
Becker W., Weber Y., Wetzel K., Eirmbter K., Tejedor F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 36; DB 1; Length 473; 71.4%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570E0E08A51C8460 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding; Transferase; Nucleotidy Lransferase.
DOMAIN 435 473 UBIQUITIN-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.4%; Pred. ...
                                                                                                                                                                                                                                                                                                               Pfam; PF00240; ubiquitin; 1.
PROSITE; PS00813; 25A_SYNTH_1; FALSE_NBG.
PROSITE; PS00813; 25A_SYNTH_2; 1.
PROSITE; PS50152; 25A_SYNTH_3: 1.
PROSITE; PS50152; 25A_SYNTH_3: 1.
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                                                                                                                                                                                                                         MGD; MGI:1344390; Oasl. InterPro; IPRO01797; 25A_synth. InterPro; IPRO01201; PAP_25A_core. InterPro; IPRO00626; Ubiquitin.
                                                                                                                                                                                                    EMBL; AF068835; AAD02818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA; 54625 MW;
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Matches 5; Conservative
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| 109 KKRLIHC 115
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Q92630;
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InterPro; IPR002290; Ser_thr_pkinase.
Ffam; PF00069; pkinase; 2.
SMART; SM00220; STRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
ATP-binding; Phosphorylation.
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SEQUECE FROM N.A.
STRAIN-CV. PETO 238R; TISSUB-Leaf;
STRAIN-CV. PETO 238R; TISSUB-Leaf;
MEDLINE-96421572; PubMed-8824220;
Gu Y.O., Chao W.S., Walling L.L.;
"Localization and post-translational processing of the wound-induced leucine aminopeptidase proteins of tomato.";
T Biol. Chem. 271:25880-25887(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDIINE=94052201; PubMed=8234334;
MEDIINE=94052201: PubMed=8234334;
MEDIINE=94052201: PubMed=8234334;
Mediinopedianse: An inducible component of the defense response in Lycopersicon esculentum (tomato).";
Proc. Natl. Acad. Sci. U. S.A. 90:9906-9910(1993).
-!- FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR TURNOVER OF INTRACELLULAR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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STRAIN-CV. VF36; TISSUE-Pistil;
MEDLINE-95375233; Pubmed-7647301;
Milligan S.B., Gasser C.S.;
"Nature and regulation of pistil-expressed genes in tomato.";
Plant Mol. Biol. 28:691-711(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%; Score 33; DB 1; Length 528; 71.4%; Pred. No. 15;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 AA; 59714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE OF 103-571 FROM N.A.
                                                                                                                                                       EMBL, Y13493; CAA73885.1; -. EMBL; Y09216; CAA70418.1; -. HSSP; Q16539; IWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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268 KNRIIHC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KKRILHC 7
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WOUNDING
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48 KRIVHC
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ACT_SITE
SEQUENCE
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AMPL_SOLTU
STANDANCE.

DAMPL_SOLTU
STANDANCE.

AC P31427;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1996 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DT aninopeptidase, chloroplast precursor (EC 3.4.11.1) (Leucine DE aminopeptidase) (LAP) (Leucyl aminopeptidase) (Prolyl aminopeptidase)

THE C 3.4.11.5) (Prolyl aminopeptidase).

Streptophyta; Embryophyta; Tracheophyta;

Streptophyta; Core eudicots;

The C 3.4.11.5 (Relation).

Streptophyta; Core eudicots;

The C 3.4.11.5 (Relation).

The C 3.4.11.5 (Relation).
                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
-!- COFACTOR: BINDS TWO ZING LONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                               -i- INDUCTION: BY WOUNDING.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17; ALSO KNOWN AS THE CYTOSOL AMINOPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                 Aminopeptidase; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA.
ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
R -> G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 571;
26;
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T -> S (IN REF. 3).

T -> L (IN CLONE PBLAP2).

C7A224837E73939D CRC64;
                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL)
AMINOPEPTIDASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                Pfam; PF00883; Peptidase_Ml7; 1.
Pfam; PF02883; Peptidase_Ml7; 1.
Pfam; PF02789; Peptidase_Ml7_N; 1.
PRINTS; PR00481; LANNOPTDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
Transit peptide; Chloroplast; Aminope; TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60279 MW;
                                                                                                                                                                                                                     EMBL; U50151; AAC49456.1; -. EMBL; U50152; AAC49457.1; -. EMBL; U20593; AAA80498.1; -. HSSP; P00727; 1LAM.
MEROPS; M17.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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KRIVHC 53
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ACT_SITE
ACT_SITE
VARIANT
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Best Local
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STRAIN=CV. DESIREE; MEDLINE-94339796; PubMed-7765119;

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                                                                                                                                                                                                                                                                 STRAIN=CV. DESIREE; TISSUE=Leaf;
MEDLINE=93005746; PubMed=1392612;
Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
Willmitzer L., Prat S.;
"General roles of abscisic and jasmonic acids in gene activation as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; Irruccol, 1.
Pfam; PF00883; Peptidase_M17; 1.
Pfam; PF02089; Peptidase_M17_N; 1.
PRINTS; PR00681; LANNOPPDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
Transit peptide; Chloroplast; Aminopeptidase; Hydrolase; Zinc.
TRANSIT 1 53 CHLOROPLAST (POTENTIAL).
TRANSIT 1 573 AMINOPETIDASE.
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Herbers K., Prat S., Willmitzer L.;
"Functional analysis of a leucine aminopeptidase from Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN LEAVES, TO A LESSER EXTENT IN STEMS, BUT NOT IN ROOTS. INDUCTION: BY ABSCISIC ACID (ABA), JASMONIC ACID (JA) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3152145A4A7FB291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               925 AA.
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                                                                                                                                                                                                                              result of mechanical wounding.";
Plant Cell 4:1157-1170(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X77015; CAA54314.1; -. EMBL, X77045; CAA48038.1; -. PIR; S24769; S24769. PIR; PQ0470; PQ0470.
                                                                                                       SEQUENCE OF 19-573 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.08;
                                                            lanta 194:230-240(1994).
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342
347
427
427
429
354
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Matches 5; Conserv
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342
347
427
429
354
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111: 11
34 KKRVDHC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KKRILHC 7
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                                                                                                                                                                                                                                                                                                                                                              HSSP; P20081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKB2_HUMAN P26885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                      STRAIN=S288C / A8972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avilles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
FK50Mobinding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (EC 5.2.1.8).
FKBP2 OR FKBP13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Russnak R., Pereira S., Platt T.; "RNA binding analysis of yeast REF2 and its two-hybrid interaction with a new gene product, FIR1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse),
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
           01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Polymerase-interacting protein 1 (Factor interacting with REF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                            with a new gene product, FIRL.";
Gene Expr. 6:241-258(1996).
-!- FUNCTION: Interacts with poly(A) polymerase and with REF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 32; DB 1; Length 925; 71.4%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                      del Olmo M., Gross S., Moore C.L.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              925 AA; 104701 MW; 707D9839EE31322B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> P (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE-97339480; PubMed-9196079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U17262; AAB46625.1; -. EMBL; U18778; AAB64565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 71.4%;
5; Conservative
                                                               PIPI OR FIR1 OR YER032W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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SGD; SO000834; FIR1.
CONFLICT 663 6
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841 KKRLSHC 847
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                                                                                                                                                         STRAIN-W303;
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P45878;
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                                                                                                                                             "Structural organization of the genes encoding human and murine FKS06-binding protein (FKBP) 13 and comparison to FKBPI."; FKS06-binding protein (FKBP) 13 and comparison to FKBPI."; Gene 134:271-275(1993).
-!- FUNCTION: PPIasses accelerate the folding of proteins. May function as a component of membrane cytoskeletal scaffols.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FKSGO6-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans
isomerase) (PPiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 140 PREVENT SECRETION FROM ER (POTENTIAL).
140 AA; 15344 MW; F4E7FCC7766A0416 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      -:- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
-:- SUBNIT: Interacts with the C-terminal domain of 4.1G.
-:- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).
-:- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Colon carcinoma;
MEDLINE-91319747; PubMed=1713687;
Jin Y.-J., Albers M.W., Lane W.S., Bierer B.E., Schreiber S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
STRAIN-129/SVJ; TISSUE-Liver;
MEDLINE-94085790; PubMed-7505249;
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a membrane-associated human FK506- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%; Score 31; DB 1; Length 140; 71.4%; Pred. No. 11; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95542; FKbp2.
InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
PROSITE; PS00454; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS50059; FKBP_PPIASE_2; 1.
ISOMERASE; Rotamase; Signal; Endoplasmic reticulum.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FK506-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rapamycin binding protein, FKBP-13.";
Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AA
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                                                                                                              Burakoff S.J., Dilella A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M77831; AAA37631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latrelle P., Louis B.J., Macri C., Mardis B., Menezes S., Mouser L., Mhan M., Rifkin L., Riles L., St Peter H., Trevaskis B., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                            "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 144 AA; 16678 MW; 1ABB9491523EEA89 CRC64;
                                                                                                                                                                                                                                                               EMBL; U00060; AAB68924.1; -.
                                                                                                         Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                               PIR; S46716; S46716.
SGD; S0001137; YHR095W.
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
'-hnc 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 KKRILH 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKRILH 6
                                                                                                                                                                                                                                                                                                                                                                                                                     1 KKRILH
                                                              Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              MEDLINE=93112052; PubMed=1281998; Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.; "Chromosomal band assignments of the genes encoding human FKBP12 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAIN-S28BC / AB972;
STRAIN-S28BC / AB972;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREVENT SECRETION FROM ER (POTENTIAL)
                                                                       Biochem. Biophys. Res. Commun. 189:819-823(1992).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism. SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 16.7 kDa protein in HXTI-HXT5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.5%; Score 31; DB 1; Length 141; 71.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                  ASSOCIATED (PROBABLE).
-1 TISSUE SPECIFICITY: T-CELLS AND THYMUS.
-1 SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9F4751CA7D82D064 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FK506-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> A.
/FTId~VAR_006411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S -> TA.
/FTId=VAR_006410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y -> C.
/FTId=VAR_006412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00453; FKBP_PPIASE_1; 1. PROSITE; PS00454; FKBP_PPIASE_2; 1. PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AA; 15654 MW;
                                                                                                                                                                                                                                                                                                                                                     EMBL; M65128; AAA58473.1; -.
EMBL; M75099; AAA36563.1; -.
PIR; JC1365; JC1365.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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141
21
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MIM; 186946; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
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35 KKRVDHC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KKRILHC 7
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P38808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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YHP5_YEAST
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Gaps

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77.5%; Score 31; DB 1; Length 144; 100.0%; Pred. No. 11; 0; Indels Live 0; Mismatches 0; Indels

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                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
; 2A2A667672A8328A CRC64;
YZG1_CAEEL STANDARD; PRT; 257 AA.
P55326; Q19405.
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
F19-0CT-2001 (Rel. 40, Last annotation update)
F136-0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 AA; 28696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 268105; CAA92122.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKRILHC 7
| ||:||
88 KTRIVHC 94
                     NCBI_TaxID=727;
                                                                                                                                                                                                influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                TIGR; HI0624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
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YD2H_SCHPO
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                                                                                                                                                                                                                   Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.; "Sequencing and functional analysis of a 32.560 bp segment on the left arm of yeast Chromosome II. Identification of 26 open reading frames, including the KIPl and SEC17 genes."; yeast 9:1355-1371(1993).
                                                                                                                                                                                                                                                                                                                                                                         MOI. Cell. Biol. 15:2037-2050(1995).
-1- FUNCTION: DIRECT OR INDIRECT POSITIVE REGULATOR OF GLC7 ACTIVITY.
-1- SIMILARITY: CONTAINS 1 UBX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               MEDLINE=95198723; PubMed=7891699;
Zhang S., Guha S., Volkert F.C.;
"The Saccharcomyces SHP1 gene, which encodes a regulator of
phosphoprotein phosphatase 1 with differential effects on glycogen
metabolism, melotic differentiation, and mitotic cell cycle
                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 AA; 46987 MW; AB46C88D7ED4F11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
SUN protein (FMU protein).
                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                             423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                      SHP1 protein.
SHP1 OR YBL058W OR YBL0515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                              PRT;
                                                                                                                                                                                                          MEDLINE-94205266; PubMed-8154187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 223261; CAA80789.1; -.
EMBL; 235819; CAA84878.1; -.
PIR; S39830; S39830.
PIR; S37331; S37331.
SGD; S0000154; SHP1.
InterPro; IPR001012; UBX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00789; UBX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1::|||
359 KREVLHC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00166;
                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                          DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KKRILHC 7
                     RESULT 12
SHP1_YEAST
ID SHP1_YEAST
AC P34223;
                                                                  01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUN_HAEIN
P44788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
SUN_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OS OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
SEQUENCE FROM N.A.
STRAIN=RD, KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
MCKennen R.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE SUN (BACTERIAL) / NUCLEOLAR PROTEIN NOL1/NOP2 (EUKARYOTES) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pearson D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YD2H_SCHPO STANDARD; PRT; 560 AA. 610264, 013899; 010-067-1996 (Rel. 34, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Hypothetical 63.1 kDa protein C56F8.17C in chromosome I. SPACS6F8.17C or SPAC22A12.01C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50597 MW; D91FAB88FFDE34B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 1;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; FPR01678; No11_Nop2_Sun.
InterPro; IPR000139; NusB.
InterPro; IPR000139; NaM_bind.
Pfam; PF01189; No11_Nop2_Sun; 1.
Pfam; PF01029; NusB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD005242; NusB; 1.
PROSITE; PS01153; NOL1_NOP2_SUN; 1.
Complete proteome.
SEQUENCE 451 AA; 50597 MW; D91F!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32745; AAC22284.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-105 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
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NA KW
KW
SO FT
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   ö
Pearson D., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST SNM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERSINE NO. TRUE 1907;

MEDILINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L. T., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496512(1995).

-!- FUNCTION: REP HELICASE IS A SINGLE-STRANDED DNA-DEPENDENT ATPASE INVOLVED IN DNA REPLICATION; IT CAN INITIATE UNWINDING AT A NICK IN THE DNA. IT BINDS TO THE SINGLE-STRANDED DNA AND ACTS IN A PROGRESSIVE FASHION ALONG THE DNA IN THE 3' TO 5' DIRECTION (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                           Length 560;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                     63076 MW; BF4BDE8C28EAD227 CRC64;
                                                                                                                                                                                                                                                                                                                         Score 31; DB 1;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
ATP-dependent DNA helicase rep (EC 3.6.1..).
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                         77.5%;
                                                                                                                                                                                                                          EMBL; 299295; CAB16571.2; -. EMBL; 269728; CAA93588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32748; AAC22309.1; -. HSSP; P09980; 1UAA.
                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 560 AA; 6
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           :1:111
295 RRVLHC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                     2 KRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P09980;
TIGR; HI0649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR HI0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REP_HAEIN
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
REP_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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DR InterPro; IPR000212; UvrD-helicase.

DR Pfan, PF00580; UvrD-helicase.

KW Hydrolase; Helicase; DNA replication; ATP-binding; DNA-binding;

KW Complete proteome.

FT NP_BIND 22 ATP (POTENTIAL).

SQ SEQUENCE 670 AA; 77745 MW; 802A131251ED4E24 CRC64;

Query Match

Best Local Similarity 83.3%; Pred. No. 50;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 2 KRILHC 7

:|||||||

Db 281 QRILHC 286

Search completed; November 1, 2002, 14:47:49

Job time: 1.36013 secs
```

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 1, 2002, 14:43:58; Search time 0.742765 Seconds Run on:

(without alignments) 905.569 Million cell updates/sec

US-09-606-129A-34 40 1 KKRILHC 7 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Post-processing: Minimum Match 08

Listing first 45 summaries

PIR_71:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	biliverdin reducta	biliverdin reducta	biliverdin reducta	hypothetical prote	٦			hypothetical prote	02	1-phosphatidylinos	C6 protein - rabbi	al	Ø		transposase all197			$\sim$	cyclin delta-2 - A				leucyl aminopeptid	hypothetical prote	hypothetical prote	hypothetical prote	шешр	binding protein -	FK506/rapamycin-bi
SUMMARIES	GI	G02066	S62624	A42268	н86206	T04537	T02486	C86463	T46904	F85015	T01723	H41700	A38117	AD2414	AE2064	AF2052	AF2152	AG1875	AG2037	S51651	T07850	T07047	T07849	S41376	S50490	T01020	T07474	AI0092	149668	JC1365
	08	7	7	7	7	7	7	7	7	7	~	7	7	7	7	7	7	~	~	~	~	۲3	~	Н	~	7	7	~	~	7
	Length	296	296	295	512	633	208	497	137	401	431	144	189	189	189	189	189	189	189	383	266	571	571	573	925	1257	42	100	140	142
đ	Query	100.0	100.0	95.0	95.0	95.0	87.5	85.0	82.5	82.5	82.5	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	77.5	77.5	77.5	77.5
	Score	40	40	38	38	38	35	34	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31
	Result No.		7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote	protein F13E6.1   1 hypothetical prote		interferon-induced	interferon-induced	hypothetical prote	CDS protein F9L11.	hypothetical prote	NADH dehydrogenase	helicase (EC 3.6.1	hypothetical prote	hypothetical prote	cappuccino gene pr
S46716 F75189	E89632 S39830	F64155	JC4775	A56534	T22440	E86453	T38927	T11629	D64084	T34444	T22442	T13286
77	0 0		4 (4	7	7	~	7	7	7	7	7	7
144 145	257 423	451	504	504	508	522	539	551	698	707	817	1058
77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5
31	31	31	31	31	31	31	31	31	31	31	31	31
30	3.2 3.3	34	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  G02066  B011verdin reductase (EC 1.3.1.24) - human N;Alternate names: biliverdin IX-alpha reductase C1:Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998 C;Accession: G02066 R;Komuro, A.; Tobe, T.; Nakano, Y.; Yamaguchi, T.; Tomita, M. Submitted to the EMBL Data Library, August 1995 A;Reference number: H00768 A;Reference number: H00768 A;Reference number: H00768 A;Reference number: H00768 A;References: EMBL: U34877; NID:g1143231; PID:g1143232 C;Keywords: oxidoreductase C;Keywords: oxidoreductase Ouery Match Best Local Similarity 100.0%; Score 40; DB 2; Length 296; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps	1 KKRILHC 7
RESULT 1 02006 billowedin NAlternate C.Species: C.Date: 21- C.Accession R.Komuro, A Submitted t A.Reference A.Accession A.Status: A.Status: A.Residues: A.Residues: A.Cross_ref C.Keywords: C.Keywords: Query Mat Best Loca Matches	Oy 1 K

1111111 275 KKRILHC 281 Q ò

RESULT 2

ö

Diliverdin reductase (EC 1.3.1.24) - human
N;Alternate names: biliverdin IX-alpha reductase
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
C;Accession: S62624; S62622; S29736
R;Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Blochem. 235, 372-381, 1996
A;Title: Humann biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A;Reference number: S62622; MUID:96202961
A;Accession: S62624 A;Molecule type: mRNA A;Residues: 1-296 <MAI> A;Cross-references: EMBL:X93086; NID:g1246748; PIDN:CAA63635.1; PID:g1246749 A;Accession: 562622

A; Molecule type: protein
A; Residues: 3-24, X', 26-27, X', 29-36;48-74;228-234;235-248 <MAF>
R; Residues: 3-24, X', 26-27, X', 29-36;48-74;228-234;235-248 <MAF>
R; Residues: 3-24, X', 26-27, X', 29-36;48-74;228-234;235-248 <MAF>
A; Title: Purification and characterization of human biliverdin reductase.
A; Reference number: \$29736; MUID:9314333
A; Reference number: \$29736; MUID:93143333
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 3-24, X', 26-27, X', 29-36;48-74;228-234;235-248 <MAW>
A; Note: the sequence of peptide 1 from page 323 seems not to belong to this protein

```
A; Accession: Trustated from GB/EMBL/DDBJ
A; Accession: Trustated from GB/EMBL/DDBJ
A; Scatus: translated from GB/EMBL/DDBJ
A; Roceleter cos: EmbL: AccOu4680; NID: 93420052
A; Residues: 1-508 < ROU>
A; Experimental source: cultivar Columbia
R: Lin, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487
A; Settus: preliminary
A; Molecule type: DNA
A; Residues: 1-508 < STO>
A; Residues: 1-508 < STO>
A; Cross-references: GB:AE002093; NID: 93420052; PIDN:AAC31853.1; GSPDB:GN00139
                                                                                                                                                                                                                      hypothetical protein F28J12.70 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.) bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999 (C.) Accession: T04537 (C.) Accession: T05537 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein At2g29990 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F23F1.9 [c;Species: Arabidopsis thaliana (mouse-car cress) [c;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02486; B84703 [F;Rounasley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 87.5%; Score 35; DB 2; Length 508; Local Similarity 71.4%; Pred. No. 17; es 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL021710
A;Experimental source: cultivar Columbia; BAC clone F28J12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 158/3; 230/1; 283/3; 305/3; 360/2; 398/3; 458/3
C;Superfamily: NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; Di
Pred. No. 5;
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85.7%;
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A; Accession: T02486
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A;Gene: At2g29990; F23F1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 215377
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A; Residues: 1-633 <BEV>
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    236 KKRLLHC 242
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591 KKRIMHC 597
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236 KRRLLHC 242
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Razzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome l of the plant Arabidopsis.
A.Reference number: A86141; MuID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diliverdin reductase (EC 1.3.1.24) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A42268
R;Fakhrai, H.; Maines, M.D.
J. Biol. Chem. 267, 4023-4029, 1992
A;Title: Expression and characterization of a CDNA for rat kidney biliverdin reductase. A;Reference number: A42268; MUID:92156147
A;Reference number: A42268
A;Reference compared with conceptual translation
A;Residues: 1-295 cFAK>
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A;Cross-references: GB:AE005172; NID:g8954028; PIDN:AAF82202.1; GSPDB:GN00141
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                 A;Gene: BVR
C;Keywords: oxidoreductase
F;3-296/Product: biliverdin reductase IX-alpha #status experimental <MAT>
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A.Note: sequence extracted from NCBI backbone (NCBIP:82800)
C.Keywords: liver; oxidoreductase
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Pred. No. 2.5;
1; Mismatches (
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1; Mismatches
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6; Conservative
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Best Local Similarity 85./.
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A; Residues: 1-512 <STO>
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274 KKRIMHC 280
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C;Genetics:
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N.Alternate names: protein A_IG002N01.9
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C.Accession: T01723
R.Schet, P.; Maggi, L.
Submitted to the EMBL Data Library, June 1997
A.Description: The sequence of A. thaliana IG002N01.
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A:Introns: 40/2; 94/3; 161/3; 224/2; 255/1; 271/1; 303/1; 339/2
A:Note: A_IG002N01.9
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A;Experimental source: cultivar Columbia
C;Genetics:
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A; Reference number: A85001; MUID:20083488
A; Accession: F85015
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <SCH>
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 4; Conserv
                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <STO>
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Best Local Similarity
Matches 6; Conserv
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73 KKNVIHC 79
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                                      uypothetical protein T3M13.4 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: C66463
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C;Accession: C66463
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.E.; Hughes, B.; Huizar, L.
ansen, N.F.; Hughes, B.; Huizar, L.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.Y.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome I of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719
A;Rodecule type: DNA
A;Residues: 1-497 < STO>
A;Cross-rafez-nea
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C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Accession: 146904
A:Status: Dreliminary
A:Accession: 146904
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <AAA>

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C;Genetics:
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85.7%; Pred. No. 14;
ive 0; Mismatches 1; Indels
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Pred. No. 27;
1; Mismatches 0; Indels
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83.3%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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63 KKRKLHC 69
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| 434 KRVLHC 439
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Job time : 1.90943 secs
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                                                                                                                        Query Match
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AF2052
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                                                                                                           R.Alam, J.; Vrba, J.W.; Cai, Y.; Martin, J.A.; Weislo, L.J.; Curtis, S.E. J. Bacteriol. 173, 5778-5783, 1991
J. Bacteriol. 173, 5778-5783, 1991
A. Title: Characterization of the IS895 family of insertion sequences from the cyanobacte A; Reference number: A38117; MUID:91358370
A; Reference number: A38117; MUID:91358370
A; Reference number: A38117
A; Molecule type: DNA
A; Residues: 1-189 <ALA>
A; Cross-references: GB:M67475; NID:9142026; PIDN:AAA98138.1; PID:9142027
A; Cross-references: GB:M67475; NID:9182026; PIDN:AAA98138.1; PID:9142027
A; Cross-references: GB:M67475; NID:9182026; PIDN:AAA98138.1; PID:9142027
A; Mobile element: insertion sequence IS895
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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminary
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C; Species: Anabaena sp. (strain PCC 7120)
C; Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C; Accession: AE2064
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A; Aitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; WUID:21592285; PMID:11759840
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A;Residues: 1-189 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76567.1; PID:g17134005; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                            C;Species: Anabaena sp.
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 15-Oct-1999
C;Accession: A38117
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hypothetical protein 1 - Anabaena sp. insertion sequence IS895
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Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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transposase all1972 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AF2052
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata A, 7itle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
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0
A;Status: preliminary
A;Notatus: preliminary
A;Motacule type: DNA
A;Residues: 1-189 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73766.1; PID:g17131158; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a112067
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A;Molecule type: DNA
A;Residues: 1-189 <KRR>
A;Cross-references: GB:BA000019; PIDN:BAB73671.1; PID:g17131062; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1972
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                                                                                                                                                                                                Score 32; DB 2;
Pred. No. 29;
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Pred. No. 29;
                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                80.0%;
71.4%;
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ilarity 71.4%;
Conservative
                                                                                                                                                                                                                         Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
5; Conserv
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171 KKRLKHC 177
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Sequence 14, App
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Sequence 2, App
Sequence 4, App
Sequence 2, App
Sequence 2, App
Sequence 1, App
Sequence 166, App
Sequence 166, App
Sequence 166, App
Sequence 166, App
                    Sequence 7
                                                                                                                                                                                                                                                                                  APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
US-08-469-423-5
US-08-669-4438-5
US-08-469-427A-7
US-08-669-427A-7
US-08-569-632-7
US-08-835-170-4
US-08-835-170-4
US-08-835-170-2
US-08-835-170-2
US-08-835-170-2
US-08-959-257-4
US-08-969-106-6
US-08-969-166-6
US-08-444-631-166
US-08-444-631-166
US-08-851-843A-200
US-08-851-843A-14
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Pred. No. 13;
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                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPAX: 312-913-0001
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97,837
                                                                                                                                                                                                                                                     Sequence 5, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 269 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 5; Conserv
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KRRMLHC 73
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                                                                                                                                                                                                                                            US-09-006-783A-5; Sequence 5, App
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Sequence 10, Appl
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292.168 Million cell updates/sec
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                                                                    November 1, 2002, 14:44:48; Search time 0.585209 Seconds
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Sequence 2, Ap
Sequence 2, Ap
Sequence 5, Ap
Sequence 19, A
Sequence 19, A
Sequence 6, Ap
Sequence 6, Ap
Sequence 6, Ap
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
          GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-499-082-10
US-09-006-7818-33
US-09-659-166-2
US-08-892-770-5
US-08-892-770-5
US-08-892-770-5
US-08-892-770-5
US-08-892-770-5
US-08-332-966B-4
US-08-336-618-19
US-08-333-618-19
US-08-803-99-6
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US-08-569-063C-3
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                                                                                                                                                                                                                                                                Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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40
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Match 1
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Patent No. 6143522
GENERAL INFORMATION:
APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 1DM. COSTAINS SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082 FILING DATE: CLASSIFTCATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158 FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US/08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION NUMBER: US/08/751230
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: US/08-DEC-1995
FILING DATE: US/08-DEC-1995
                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 1.05/08/751,230 FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 14;
2; Mismatches
                                                                                                  CULLING DATE: 15-NOV-TO FILING DATE: 15-NOV-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.0
Best Local Similarity 71.4
Matches 5; Conservative
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                            OPERATING SYSTEM:
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82 KRRMLHC 88
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COMPUTER:
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US-09-499-082-10
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING!
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Garkavtsev, 1gor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-1404

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURREW APPLICATION DATA:

APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                                  Sequence 10, Application US/09258371
Patent No. 5986078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MOOL, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02877
TELECOMMUNICATION INFORMATION:
TELEFAN: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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Best Local Similarity 71.4.
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ZIP: 22313-1404
COMPUTER READABLE FORM:
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                      RESULT 2
US-09-258-371-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-751-230-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
APPLICANT: Raidowol, Karl
TITLE OF INVENTION: p33/INC1 as a Mediator of p53 Signaling
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 200 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 4; Length 294;
Pred. No. 14;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CREASY, CARETHA LEE
APPLICANT: TESTA, TANIA TAMSON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30218
CURRENT APPLICATION NUMBER: US/09/659,166
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: UK 9921505.5
PRIOR APPLICATION NUMBER: UK 9921505.5
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.5%; Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/006,783A FILING DATE: 15-JAN-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                 ; Sequence 3, Application US/09006783A; Patent No. 6297366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09659166
; Patent No. 6355465
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 294 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-006-783A-3
                                                                                                                                                                                                                                                                        ADDALOS STREET: 300 SCULL.
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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| 82 KRRMLHC 88
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                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                          US-09-006-783A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-659-166-2
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LENGTH: 527
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Pred. No. 14;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                           Query Match 85.0%; Score 34; DB 4; Length 294; Best Local Similarity 71.4%; Pred. No. 14; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  JUS-09-258-372-10

| Sequence 10, Application US/09258372
| Sequence 10, Application US/09258372
| Patent No. 6238918
| GENERAL INFORMATION:
| APPLICANT: Riabowol, Karl
| TITLE OF INVENTION: SUPPRESSOR GENE INGI
| TITLE OF INVENTION: SUPPRESSOR GENE INGI
| NUMBER OF SEQUENCES:
| ADDRESSEE: Burns, Doane, Swecker & Mathis |
| STREET: 699 Prince Street |
| CITY: Alexandria |
| STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MOOL, LESLIE A.
RECISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
SOURCECK: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-258-372-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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82 KRRMLHC 88
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82 KRRMLHC 88
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Gaps

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APPLICANT: Walling, Linda L.
APPLICANT: Walling, Linda L.
APPLICANT: Pautot, Veronique
APPLICANT: Gu, Yong-Qiang
APPLICANT: Chao, Wun Shaw
TITLE OF INVENTION: Improved Promoters for Enhancing Plant
TITLE OF INVENTION: Productivity
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 4; Length 528; Pred. No. 37;
                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,770
FILING DATE: 15-JUL-1997
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STREET: Two Embarcadero Center, Eighth Floor
TITY: San Francisco
STATE: California
                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,484
FILING DATE: 09-UNI-1999
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/802,466
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: WIlliam T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08892770 Patent No. 5962670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Quine, Jonathan A. REGISTRATION NUMBER: P-41,261
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 610-270-5219
                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.4
Matches 5; Conservative
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ZIP: 94111-3834
                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKRILHC 7
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                      1; Indels
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TITLE OF INVENTION: HUMAN PROTEIN KINASE HOACF72
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Creasy, et al.
TITLE OF INVENTION: HUMAN PROTEIN KINASE HOACF72
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMILHALINE Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,466
ELLING DATE: 19 February 1997
CLASSIFICATION: 435
                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
    Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH50002
                                                                                                                                                                                                    Sequence 2, Application US/08802466
Patent No. 5972606
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US-09-350-484-2
; Sequence 2, Application US/09350484
Sequence 0. 6159716
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: William T. Han
REGISTRATION NUMBER: 34,344
REPERDEL/DOCKET UNBER: GHE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: King of Prussia
  71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
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71.48;
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LENGTH: 528 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19 Febru
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                 | ||:||
267 KNRIIHC 273
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268 KNRIIHC 274
                                                            1 KKRILHC 7
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                                                                                                                                                              RESULT 8
US-08-802-466-2
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                sequence of acidic leucine aminopeptidase (LapAl) protein from tomato"
                                                                                                                            Length 571
        /note- "deduced full-length protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 1; Length 40; Pred. No. 8.4;
                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steven J. Burakoff
APPLICANT: Steven J. Burakoff
APPLICANT: Stuart L. Schreiber
APPLICANT: Barbara E. Bierer
TITLE OF INVENTION: FKBP-13, AN FK506-BINDING
TITLE OF INVENTION: IMMUNOPHILIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM Ps/2 Model 502 or 558X
OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/822,966B
FILING DATE: January 17, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                            DB 2;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/052001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                    1; Mismatches
                                                                                                                            Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/07822966B Patent No. 5498597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.58;
71.48;
                                                                                                                            80.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.48
Matches 5; Conservative
                                                                                                                            Query Match 80.0°
Best Local Similarity 83.3°
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
                           CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-08-892-770-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KKRVDHC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KKRILHC 7
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48 KRIVHC 53
                                                                                                                                                                                                       2 KRILHC 7
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US-07-822-966B-4
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US-08-336-618-19
                                                                                                                                                                                                                                                                                                         RESULT 12
US-07-822-966B-4
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; Sequence 5, Application US/08892770
; Patent No. 5962670
; GENERAL INFORMATION:
    APPLICANT: Walling, Linda L.
    APPLICANT: Bautot, Veronique
    APPLICANT: Gu, Yong-Qiang
    APPLICANT: Gu, Yong-Qiang
    APPLICANT: Choo, Wun Shaw
    TITLE OF INVENTION: Productivity
    NUMBER OF SEQUENCES: 13
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                    /note= "deduced partial protein sequence of acidic leucine aminopeptidase 2 (LapA2) from tomato"
                                                                                                                                                                                                                                                                                                                                                                                        Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,770
FILING DATE: 15-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 2;
Pred. No. 63;
1; Mismatches
REFERENCE/DOCKET NUMBER: 023070-072100US
TELECOMMINICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     023070-072100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                           MAME/KEY: Protein
LOCATION: 1.565
COTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: US-08-892-770-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
LOCATION: 1..571
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                                                                                                                                           TYPE: amino s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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77.5%; Score 31; DB 5; Length 99; 71.4%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/07822966B
Fatent No. 5498597
GENERAL INFORMATION:
APPLICANT: Steven J. Burakoff
APPLICANT: Steven J. Burakoff
APPLICANT: Barbara E. Bierer
TITLE OF INVENTION: FKBP-13, AN FKSO6-BINDING
TITLE OF INVENTION: IMMUNOPHILIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                              NAME: Grandan, Parricla
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00530/052001
CURRENT APPLICATION DATA:
                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0053G
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 amino acids
                                                  APPLICATION NUMBER: PO
FILING DATE: 19920507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein PCT-US92-03993-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KKRVDHC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKRILHC 7
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US-07-822-966B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                     APPLICANT: Livingston, David J.

TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 1
ADDRESSED: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 1; Length 88;
Pred. No. 18;
                                                                                                                                                                                                     ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive CITY: Learington STRATE: Massachusetts
                                                                                                                                                                                                                                                                                                             COUNTR:

2IP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING PATE: 09-NOV-1994
FILING PATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/77,752
FILING DATE: 11-0CT-1991
PRIOR APPLICATION DATE: PRIOR PAPLICATION DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPI91-06A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: VPIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-336-618-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 KKRVDHC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KKRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US92-03993-5
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0;
                                       0; Gaps
Query Match
Pest Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels
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Qy 1 KKRILHC 7 | | | | | | | | Db 35 KKRVDHC 41

Search completed: November 1, 2002, 14:51:58 Job time : 0.585209 secs

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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 14:40:53; Search time 1.58682 Seconds

(without alignments)

489.985 Million cell updates/sec

Title: US-09-606-129A-34

Perfect score: 40
Sequence: 1 KKRILHC 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Database : A_Geneseq_032802:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 1. (SIDSI)goddata/geneseq,geneseqp-embl/AA1980.DAT:*
2. /SIDSI/goddata/geneseqp-embl/AA1981.DAT:*
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9. /SIDSI/goddata/geneseqy-embl/AA1980.DAT:*
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112. /SIDSI/goddata/geneseqy-embl/AA1980.DAT:*
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114. /SIDSI/goddata/geneseqy-embl/AA1981.DAT:*
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165. /SIDSI/goddata/geneseqy/geneseqp-embl/AA1999.DAT:*
170. /SIDSI/goddata/geneseqy/geneseqp-embl/AA1999.DAT:*
181. /SIDSI/goddata/geneseqy/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT

Arabidopsis thalia Murine INGD1 isofo Murine P37ING1 pol Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human INGD1 isofor Amino acid sequenc Amino acid sequenc Human P37ING1. Ho Tumour suppressor Description AAY97245 AAY03245 AAB84700 AAY97244 AAE06676 AAY97243 AAY97242 AAG48146 AAG48145 AAG28710 AAG48144 G DB Length Query Match 1 95.0 90.0 90.0 87.5 87.5 885.0 885.0 885.0 Score Result

Amino acid sequenc	Tumour suppressor	Human p33ING1 poly	Amino acid sequenc		Drosophila melanog	Human immune/haema	Human colon cancer	Human transcriptio	Drosophila melanog	Human protein kina	Human YAK1 (hYAK1)	Amino acid sequenc	A human alpha-2 ma	A human alpha-2 ma	=	Novel human diagno	A human alpha-2 ma	Novel human diagno	Novel human diagno	ü	Acidic leucine ami	Acidic leucine ami	Bovine FKBP-13 1mm	colon can	Novel human diagno	Bovine RFKBP. Bos	Human secreted pro	Human immune/haema	Bovine mammary tis	<u>-</u>	Novel human secret	Bovine P58 protein	Novel human diagno
AAB84698		AAW79675		AAB84697				ABB50167	ABB62446	AAW64559	-			AAG6355		ABG21224		ABG14241	ABG11998	AAB25386				-	ABG2073	-	AAG03758	-	AAB87656	-	-	-	ABG09790
22	18	19	20	22	22	22	21	22	22	19	22	21	22	22	22	22	22	22	22	77	20	20	17	22	22	13	21	22	22	17	22	18	22
279	294	294	294	294	455	82	141	350	398	528	528	549	882	899	912	1475	1508	83	126	158	565	571	40	83	93	66	104	122	137	141	182	504	504
85.0	85.0	85.0									82.5		82.5				82.5					80.0				7.		7	7	77.5	7.	7.	77.5
34	34	34	34	34							33											32				31	31	31		31	31	31	31
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34.	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana protein fragment SEQ ID NO: 34031. AAG28710 standard; Protein; 285 AA 99US-0123180. 99US-0123548. 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128714. 99US-0129845. 99US-0130077. 99US-0130449. 25-FEB-2000; 2000EP-0301439 99US-0121825 (first entry) Arabidopsis thaliana EP1033405-A2. 08-APR-1999; 16-APR-1999; 19-APR-1999; 21-APR-1999; 17-OCT-2000 25-FEB-1999; 05-MAR-1999; 01-APR-1999; 06-APR-1999; 09-MAR-1999 23-MAR-1999 25-MAR-1999 06-SEP-2000 AAG28710; RESULT 1 AAG28710 

9US - 0130510 9US - 01308910 9US - 0131449 9US - 0132407 9US - 0132485 9US - 0132485 9US - 0132486 9US - 0132486 9US - 0132486 9US - 0132486 9US - 0132487 9US - 0134218	990S-0134941. 990S-0134941. 990S-013533. 990S-013523. 990S-013622. 990S-0136782. 990S-013728. 990S-013728. 990S-013724. 990S-0138840. 990S-0138847. 990S-0139452. 990S-0139453. 990S-0139453. 990S-0139455. 990S-0139455.	90S - 0139462 90S - 0139463 90S - 0139463 90S - 0139893 90S - 0140893 90S - 0140893 90S - 0140823 90S - 0140823 90S - 0140823 90S - 0140823 90S - 0140823 90S - 01412803 90S - 01412803 90S - 0141284	10S - 0142920 10S - 0142920 10S - 0143972 10S - 0144065 10S - 0144085 10S - 0144085 10S - 0144325 10S - 0144333 10S - 0144333 10S - 0144333 10S - 0144333
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ING1. Functional cooperation between ING1 and p53 suggested that

ING2 encoded a tumour suppressor protein that functioned within the
p53 pathway. This data suggested a possible role for ING1 in head
and neck cancers and chromosomal location of the ING1 placed it
within a region that is frequently rearranged in head and neck
cancers. Large scale analysis of tumours involving ING1 has not
revealed mutations in ING1 nor significant variations in its
cancer clology. However, alternative initiation exons of the ing1
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cancer clology. However, alternation of those expressing wild type p53 p37TNG1 is able to cause
proliferation or transformation of those cells. Thus detecting a
cucleic acid encoding exon ib of ing1 by phybridisation with an
coloring coloring exon ib of ing1 by phybridisation with an
coloring coloring exon ib of ing1 by phybridisation with an
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                                                                                                                                                                                                                                                                                                                                                                                                                                      or its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 36; DB 21; Length 94; 71.4%; Pred. No. 8.8; 0; Indels ive 2; Mismatches 0; Indels
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N-PSDB; AAA53790.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p53; tumour; cancer; detection; antibody; hybridisation; exon 1b, 1NG1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB
Pred. No. 10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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                                                                99US-0160741.
99US-0160767.
99US-0160768.
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99US-0160814.
99US-0160815.
99US-0160980.
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99US-0161405.
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85.7%;
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99US-0161993
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21-OCT-1999;
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22-OCT-1999;
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                        14-0CT-1999,
18-0CT-1999,
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18-JUN-1999;
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28-APR-1999;
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04-MAY-1999;
05-MAY-1999;
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02-JUL-1999;
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                                                                                                                                                                          the p53 pathway occurs in a much larger proportion of tuncurs. In many cases the mechanism of functional inactivation of tuncurs. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with 10G1. Functional cooperation between 1NG1 and p53 suggested that in NG1 encoded a tumour suppressor protein that functioned within the p53 gaptemay. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etology. However, alternative initiation exons of the ing1 gene, each having their own promoter have been discovered...

Expression of one promoter (la) produces a protein having an identical C-terminal fragment to ING1 but an additional lot N-terminal amino acids. The newly discovered protein has been characteristics of an oncogene. When overexpressed in cells (even those expressing wild type: p331NG1). p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even proliferation or transformation of those cells: Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of these cells. Thus detecting a proliferation or transformation of the cells of the part of the cells of 
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                                                                                                             Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of
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                                Disclosure; Fig 12; 134pp; English.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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 9908-0158369
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990S-0166814
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9US - 0130449 9US - 0130810 9US - 013189 9US - 0131449 9US - 013248 9US - 0132485 9US - 0132486 9US - 0132486 9US - 0132486 9US - 0132486 9US - 0132486 9US - 0132863	9905-0134768 9905-0134768 9905-0135353 9905-0135529 9905-0136722 9905-0136782 9905-013722 9905-013722 9905-013724 9905-0137724 9905-013774 9905-013745 9905-013445 9905-013445 9905-013445 9905-013445 9905-013445 9905-013446 9905-013446 9905-013446 9905-013946 9905-013946 9905-013946 9905-013946 9905-013946 9905-013946 9905-013946 9905-013946 9905-013975 9905-013975	905 - 014 0823 905 - 014 0823 905 - 014 1842 905 - 014 2154 905 - 014 2055 905 - 014 2920 905 - 014 2920 905 - 014 2920 905 - 014 4085 905 - 014 4086 905 - 014 4086 905 - 014 4086 905 - 014 4086 905 - 014 4331 905 - 014 4333
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Pred. No. 70;
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AAG48144
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30-AUG-1999;
31-AUG-1999;
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13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
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11-AUG-1999;
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13-SEP-1999;
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23-AUG-1999;
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20-SEP-1999;
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21-0CT-1999;
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Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
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                                                                                                                                                                                                                  DB 21; Length 564;
                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human INGb1 isoform N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Figure 7a; 134pp; English.
                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                   AAY97245 standard; Protein; 94 AA
                                                                                                                                                                                                                                                 2;
             990S-0160814.
990S-0160815.
990S-0160980.
990S-0160981.
990S-0161404.
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99US-0161359.
99US-0161360.
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990S-0161920.
990S-0161992.
990S-0161993.
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71.4%;
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                   Local Similarity
nes 5; Conserv
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292 KRRLLHC 298
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21-0CT-1999;
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26-0CT-1999;
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26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                             AAY97245;
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        reveated mutations in this incl and variations in its cancer ethology. However, alternative initiation exons of the ingl cancer ethology. However, alternative initiation exons of the ingl cancer ethology. However, alternative initiation exons of the ingl gene, each having their own promoter have been discovered.

Expression of one promoter (la) produces a protein identical to inGl. Expression of a second promoter (lb) produces a protein having on identical Crterminal fragment to ING1 but an additional 104 in designated p37ING1 (Wild type: p331NG1). p37ING1 has the designated p37ING1 (Wild type: p331NG1). p37ING1 has the those expression wild type p33) p37ING1 is able to cause those expression or transformation of those calls. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid maving the sequence of exon 1b of ing1 is solated nucleic acid maving the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 or terminal peptide of p37ING1 can also be used in detection methods for the p37ING1 variant.

The polypeptides may be useful in gene therapy for treatment of cell profileration disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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 significant variations in its
                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 21; Length 94; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of the human p28-ING1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY03245 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 61; 64pp; English.
 mutations in ING1 nor
                                                                                                                                                                                                                                                                                                                                                                                             85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                 Gudkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of p33-ING1 peptides
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                                                                                                                                                                                                                                                                                                                                                                 94 AA;
                                                                                                                                                                                                                                                                                                                                    studying cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KKRILHC 7
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This is the amino acid sequence of the human p28-ING1 protein, used in the method of the invention, involving the human p33-ING1 protein. The ING1 gene encodes p33-ING1 which can be used to modulate the activity of, isolate or detect p53. Expression of the ING1 and p53 genes in a mammalian cell results in normal growth requilation anchorage-dependent growth and apoptosis as a response to irreversible DNA damage and other cellular insult. Inhibition of expression of either gene results in a loss of cellular growth confrol, anchorage independent growth, inhibition of apoptosis and resistance to radiation and cytotoxic drugs. The p33-ING1 is a component of the p53 signalling pathway that cooperates with p53 in negative regulation of cell proliferation by modulating p53 dependent component of the p53 signalling pathway can therefore be regulated (both enhanced or suppressed) by modulating p33-ING1 activity. The modulating negative regulation of restoration of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy and pathway can be required the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in anticancer therapy or for the suppression of the p53 pathway in the p53 p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 20; Length 128; . 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      defend sensitive tissues from genotoxic stress or of immortal cell lines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 83; Page 47-48; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB84700 standard; Protein; 235 AA.
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24-OCT-2000; 2000US-0602362.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA;
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67 KRRMLHC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KKRILHC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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16-AUG-2001.
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                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of human tumours and tumour cell lines, but functional inactivation of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with cremains unknown but p53 has been found to act in cooperation with NG1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter have been discovered. Cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 cancer characteristics of an oncogene. When overexpressed in cells (even characteristics of an oncogene. When overexpressed in cells (even the characteristics of an oncogene. When overexpressed in cells (even the compand of the compand to the conservation of the conservation of the cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                Gaps
a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                    p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse.
                                                                                               0;
                                                                     22; Length 235,
                                                                                             Indels
                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grigorian IA;
                                                                     DB
                                                                               Pred. No. 51;
2; Mismatches
                                                                   Score 34;
                                                                                                                                                                                                                        AAY97244 standard; Protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeremski M, Gurova KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 7a; 134pp; English.
                                                                  85.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0118941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000WO-US02959.
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                                                                                                                                                                                                                                                                                (first entry)
                                                        Ouery Match
Best Local Similarity 71.4
5. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-491278/43.
                                        235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA53792
                                                                                                                                         1:1:111
23 KRRMLHC 29
                                                                                                                          1 KKRILHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200046370-A1.
                                                                                                                                                                                                                                                                                                          Human P37ING1
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-1999;
                                                                                                                                                                                                                                                                               19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gudkov A,
                                                                                                                                                                                                                                                    AAY97244;
                                         Sequence
                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour suppressor; p471NG3; cell proliferation; cellular aging; anchorage dependence; apoptosis; tumour; cancer; gene therapy; p331NG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tumor suppressor protein p471NG3 for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis, prevention and treatment of tumours and cancers. The p47ING3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a tumour suppressor homologue protein, p331NG1 which is homologous to human tumour suppressor protein, p471NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, p471NG3, nucleic acids encoding it and antibodies against it are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 60;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  21; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour suppressor homologue protein, p33ING1.
                                                                                                                                                                                                                                                                                                                                                          DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 34;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE06676 standard; Protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA is also used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%; 5; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                  85.0%;
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity /1...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagashima M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488975/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 AA;
                                                                                                                                                                                                                                                      studying cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 KRRMLHC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200159114-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKRILHC 7
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6 14:27:58 2002

Wed Nov

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Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                    Tumour suppressor protein; p331NG1; breast cancer; brain cancer; diagnosis; therapy.
                                 AAW19119 standard; Protein; 294 AA.
                                                                                                 Tumour suppressor protein p33ING1.
                                                                                                                                                                                                                                                                             (UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Fig 3; 63pp; English.
                                                                                                                                                                                                                       96WO-CA00819.
                                                                                                                                                                                                                                                        95US-0569721
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                   Garkavstev I, Riabowol
                                                                                                                                                                                                                                                                                                                       WPI; 1997-332781/30.
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT69652
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82 KRRMLHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KKRILHC
                                                                                                                                                      Homo sapiens
                                                                                                                                                                           409721809-A1
                                                                                                                                                                                                                       36-DEC-1996;
                                                                                                                                                                                                                                            15-NOV-1996;
                                                                                                                                                                                                                                                       08-DEC-1995;
                                                                           27-AUG-1997
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                                                     AAW19119;
            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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                      AAW19119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat
                                                                                                                                         Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gure A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 22; Length 279;
Pred. No. 60;
2; Mismatches 0; Indels
                                                                                                                    Amino acid sequence of a human cancer associated antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scanlan M, Knuth A, Old L,
                                                                                                                                                                                                                                                     by AAA"
                                                                                                                                                                                                                                                                                                 /note= "Val encoded by GCA"
                                                                                                                                                                                                          /note- "Val encoded by GCG'
                                                                                                                                                                                                                                                                                                                       /note= "Ser encoded by GCT'
                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CANCER RES. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                /note- "Val encoded by
                                                                                                                                                                                                                                                                  /note= "Asp encoded
Misc-difference 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 83; Page 45-46; 62pp; English.
                                                                                                                                                                                                                                                     /note= "Asn encoded
                                                                                                                                                                                     Location/Qualifiers
                                                    AAB84698 standard; Protein; 279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1999; 99US-0451739.
24-OCT-2000; 2000US-0602362.
                                                                                                                                                                                                                                                                                                                                                                                     9-NOV-2000; 2000WO-US42334
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jager D, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-441706/47.
N-PSDB; AAH28478.
                                                                                                                                                                                                                    Misc-difference 129
                                                                                                                                                                                                                                         Misc-difference 135
                                                                                                                                                                                                                                                                Misc-difference 137
                                                                                                                                                                                              Misc-difference 123
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                                                                                                                                                                                                                                                                                                           Misc-difference
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67 KRRMLHC 73
KRRMLHC 73
                                                                                                                                                                                                                                                                                                                                           WO200147959-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KKRILHC 7
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2001.
                                                                                              17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                          AAB84698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
67
                                RESULT 12
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96US-0751230

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A full-length sequence (AAM19119) is provided of novel tumour suppressor protein p33NG1. It was deduced from a cDNA clone (AAT69652) obtd. from normal human fibroblast cells. Overexpression of p33NG1 (formerly p331G1) is thought to inhibit cell growth and DNA synthesis, probably by arresting cells in the G1 phase of the cell cycle. p331NG1 is expressed in normal mammary epithelial mammary epithelial cell lines and is not expressed in many primary brain tumours. p331NG1 can be administered to patients as a means of decreasing proliferation of cancer cells, or can be used to raise antibodies useful for the diagnosis of cancer, esp. breast
                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ING1 gene; p33ING1; human; apoptosis; cell death; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                         Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
63;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                      85.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p33ING1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
Laca 5; Conserv?
                                                                                                                                                                                                                                                                                                                                          294 AA;
                                                                                                                                                                                                                                                                                        and brain cancer
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Riabowol K;

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Human; p33-ING1 protein; growth regulation; apoptosis; DNA damage;
inhibition; anchorage independent growth; cytotoxic drug;
transcriptional activation; cancer; immortal cell line.
                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of the human p33-ING1 protein.
                                                                                                                                                                                                                                                                                                                                                AAY03244 standard; Protein; 294 AA.
                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999 (first entry)
                                                                                            WPI; 1998-542700/46.
                                                                                                                                                                                                                                                                     294 AA;
                                                                                                 N-PSDB; AAV62292
                                                                                                                                                                                                                                                                                                               |:|:|||
82 KRRMLHC 88
                                                                                                                                                                                                                                                                                                        1 KKRILHC 7
                                                         27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9916790-A1.
           Homo sapiens
                     WO9844102-A2
                                             26-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                 08-0CT-1998
                                                                                                                                                                                                                                                                     Sequence
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This is the amino acid sequence of the human p33-ING1 protein, used in the method of the invention. The ING1 gene encodes p33-ING1 which can be used to modulate the activity of, isolate or detect p53.

Expression of the ING1 and p53 genes in a mammalian cell results in normal growth regulation anchorage-dependent growth and apoptosis as a response to irreversible DNA damage and other cellular insult.

Inhibition of expression of either gene results in a loss of cellular growth control, anchorage independent growth, inhibition of apoptosis and resistance to radiation and cytotoxic drugs. The p33-ING1 is a component of the p53 signalling pathway that cooperates with p53 in negative regulation of cell proliferation by modulating p53 dependent transcriptional activation. Biological function of p53 signalling pathway can therefore be regulated (both enhanced or suppressed) by modulating p33-ING1 activity. The modulation of p33-ING1 activity can be used for the stimulation or restoration of the p53 pathway in anti cancer therapy or for the suppression of the p53 pathway to anti cancer therapy or for the suppression of the p53 pathway to immortal cell lines.
                                                                                                                                                                                                                                  (UNII ) UNIV ILLINOIS BOARD OF TRUSTEES.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 64pp; English.
                                                                                    98WO-US18179
                                                                                                                                          98US-0006783
97US-0060138
                                                                                                                                                                                                                                                                                                                       Garkavtsev I, Gudkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of p33-ING1 peptides
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-263685/22
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                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX28688
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                                                                                    24-SEP-1998;
                                                                                                                                          14-JAN-1998;
26-SEP-1997;
                              08-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of human p331NG1, a novel inhibitor of cell growth and a candidate tumour suppressor. The sequence was deduced from full-length ING1 CDNA (see AAV62285) obtained using a positive selection procedure that combined subtractive hybridisation with an in vivo selection assay to identify growth-suppressor. His expressed in normal mammary epithelial cells, but is expressed only at lower levels in several cancerous mammary epithelial cell lines and is not expressed in many primary brain capthelial cell lines and is not expressed in many primary brain cumours. A claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active p331NG1 peptide or an oligonucleotide encoding such as a peptide. A claimed method for inhibiting apoptosis in a eukaryotic cell involves administering an antisense oligonucleotide. Also claimed are a method for determining the apoptotic characteristics of a eukaryotic cell, and an isolated eukaryotic cell substantially free of p331NG1 ecil, and an isolated eukaryotic cell substantially free of p331NG1 encivity in a eukaryotic cell, and an isolated eukaryotic cell substantially free of p331NG1 eximints that may be used to induce apoptosis in eukaryotic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating eukaryotic apoptosis by increasing p331NG1 activity - using p331NG1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                        Garkavtsev I, Helbing CC, Johnston RN, Riabowol K;
brain tumour; gene therapy; tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.0%; Score 34; DB Best Local Similarity 71.4%; Pred. No. 63; Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                               (UYTE-) UNIV TECHNOLOGIES INT INC
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85.0%; Score 34; DB 20; Length 294; 71.4%; Pred. No. 63; 0; Indels Live 2; Mismatches 0; Indels
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                     Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                   Search completed: Novembook Job time: 2.58682 secs
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Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Searched:

Database

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Q9xep7 sorghum blc
055279 avian adeno
09u3d6 caenorhabd1
09u3d6 caenorhabd1
001368 drosophila
09w321 drosophila
013540 saccharomyc
09d199 mus musculu
081864 hepatitis e
0971k7 clostriolum
090zt5 xenopus lae
091k7 clostriolum
090zt5 xenopus lae
091w12 hepatitis e
094298 caenorhabd1
099w12 hepatitis e
081344 hepatitis e
081344 hepatitis e
081344 hepatitis e
081341 hepatitis e
089418 hepatitis e
069418 hepatitis e
069418 hepatitis e
069418 hepatitis e
069418 hepatitis e
069416 hepatitis e
099w15 hepatitis e
099w15 hepatitis e
099w15 hepatitis e
099w17 hepatitis e
099w18 hepatitis e
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL, BC005902, AAH05902.1;
Interpro: IPR000683; GFO_IDH_MocA.
Pfam; PF01408; GFO_IDH_MocA; 1.
SEQUENCE 296 AA; 33432 MW; A389AFDDB6ADBABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0960L4 PRELIMINARY; PRT; 296 AA. 0960L4; 1-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) UNKNOWN (PROTEIN FOR MGC:14706).
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-BRAIN, PRIMITIVE NEUROECTODERMAL;
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081862
081344
069418
069410
039221
09WLL5
09WC28
  Q9XEP7
055279
Q9U3D6
Q9U3D6
Q9W321
Q9D1Y9
Q9D1Y9
Q9D1X7
Q9D1X7
Q9D1X7
Q9D1X7
Q9D2TS
Q9D1N1
Q9D2TS
Q9D2TS
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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091116
091VZ9
09YLR1
09YK10
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Best Local Similarity 100.
Matches 8; Conservative
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1693
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289 QKYCCSRK 296
                     Q9BRW8;
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ID 09
AC 09
DT 01
DT 01
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0919p6 epizootic h
09uis5 homo sapien
09uis4 homo sapien
018233 caenorhabdi
0988f4 drosophila
098856 quillardia
015371 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q40142 lycopersico
O17778 caenorhabdi
Q9bkl4 plasmodium
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096q14 homo sapien
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045193 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              044161 caenorhabdi
                                                                                    (without alignments)
952.238 Million cell updates/sec
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                                                                        November 1, 2002, 14:43:08; Search time 1.45338 Seconds
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             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                          562222 seqs, 172994929 residues
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                                                     OM protein - protein search, using sw model
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0998F4
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09KQZ2
09JGP6
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045193
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Gapop 10.0 , Gapext 0.5
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5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
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sp_unclassified:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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2: sp_bacteria:*
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2296
7033
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234
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150
263
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1127
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385
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Gray T.A., Martone D.L., Schaldach M.A., McCarrey J.R., Nicholls R.D., "Concerted Regulation and Molecular Evolution of the Duplicated SNRPB and SNRPN loci.";
                        MEDLINE-2021376; PubMed=10770607;
MEDLINE-2021376; PubMed=10770607;
Mara E., Iwata H., Inoue T.;
The complete nucleotide sequence of segment L2 of Ibaraki virus encoding for the antiqen recognized by neutralizing antibodies.", J. Vet. Med. Sci. 62:317-321(2000).
EMBL; AB030735; BAA93692.1; -.
InterPro; IPR001742; Orbi_VP2.
Pfam; PF00898; Orbi_VP2.
Probom; PD002938; Orbi_VP2.
Probom; PB002938; Orbi_VP2.
Probom; PB002938; Orbi_VP2.
SEQUENCE 982 AA; 115598 MW; 6E347B126158F775 CRC64;
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                    77.6%; Score 38; DB 12; Length 982; 62.5%; Pred. No. 22; iive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleocapsid; Ribonucleoprotein.
SEQUENCE 234 AA; 26313 MW; A5898DB3C46A6E01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2001 (TrEMBLrel. 17, Last annotation update)
SMALL NUCLEAR RIBONUCLEOPROTEIN B.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2001 (TrEMBLrel. 17, Last annotation update)
SMALL NUCLEAR RIBONUCLEOPROTEIN B'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF134825; AAD54488.1; -...
EMBL; AF134822; AAD54488.1; JOINED
EMBL; AF134823; AAD54488.1; JOINED.
EMBL; AF134824; AAD54488.1; JOINED.
InterPro; IPR001163; SnRNP_Sm.
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Best Local Similarity 62.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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951 EKFCCGRK 958
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150 KRYCCSR 156
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STRAILNEL TOR NIG961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_raxID=666;
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008456; AAH08456.1; -.
SEQUENCE 296 AA; 33428 MW; 2CF2AA7F1CDDB707 CRC64;
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SEQUENCE 703 AA; 78488 MW; FC88B361B8A8578C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ATP-DEPENDENT HELICASE, DING FAMILY.
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Last annotation update)
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Viruses; dsRNA viruses; Reoviridae; Orbivirus.
NCBI_TaxID=10908;
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100.0%;
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EMBL; AE004261; AAF95003.1;
TIGR; VC1855; -.
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
8; Conservative
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Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 QRYCCSER 138
                                                                                                                                                                              TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QKYCCSRK 8
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Q9JGP6;
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Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Q98S56;
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Q98S56
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                   Gray T.A., Martone D.L., Schaldach M.A., McCarrey J.R., Nicholls R.D.; "Concerted Regulation and Molecular Evolution of the Duplicated SNRPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                 75.5%; Score 37; DB 4; Length 243; 71.4%; Pred. No. 11; 1.4%; Pred. 2; Mismatches 0; Indels
                                                                       Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                   Interpro: IPR001163; snRNP_Sm.
Pfam; PP01423; sm; 1.
Wholeocapsid; Ribonucleoprotein,
SEQUENCE 243 AA; 27267 MW; 05D3C4F973640CD5 CRC64;
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                                                                                         EMBL, AF134825, AAD54489.1;
EMBL, AF134822, AAD54489.1; JOINED.
EMBL, AF134823; AAD54489.1; JOINED.
EMBL, AF134824; AAD54489.1; JOINED.
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MEDLINE-99069613; Pubmed-9851916;
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Science 28:2012-2018(1998).
EMBL; 299281; CAB16509.1; -.
InterPro; IPR002900; DUF38.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                       ilarity 71.4%;
Conservative
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09V8F4;
01-MAY-2000 (TFEMBLFel. 13,
01-MAY-2000 (TFEMBLFel. 13,
01-MAY-2000 (TFEMBLFEL. 13,
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Best Local Similarity 62.37
S. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                       Local Similarity
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SEQUENCE FROM N.A.
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192 RKYCCPRR 199
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150 KRYCCSR 156
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CG14503.
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                                                   and SNRPN
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Q9V8F4
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018233
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Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Radams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Radams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Radicons R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Felifer B.D.,

Rad Baradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Felifer B.D.,

Rad Ballew R.M., Basa N., Baxendals J., Bayaktaroglu L., Basaley E.M.,

Rad Ballew R.K., Basua A., Baxendals B.P., Bhandari D., Bolshakov S.,

Rad Borkova D., Botchan M.R., Bulter H., Cadleu E., Center A., Chandra I.,

Rad Borkova D., Botchan M.R., Bulter H., Cadleu E., Center P., Chandra I.,

Rad Borkova D., Botchan M.R., Bulter H., Cadleu E., Center P., Chandra I.,

Rad Borkova D., Botchan M.R., Bulter H., Cadleu E., Center P.,

Rad Borkova D., Botchan M.R., Bulter H., Cadleu E., Center P.,

Rad Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Rad Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Rad de Pablos B., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Rad de Pablos B., Delcher A., Downes M., Durann-Rocha S., Dunkov B.C., Dunn P.,

Rad Goods A., Gong F., Gorrell J.H., Gu S., Celbart W.M., Glasser K.,

Rad Rosiner C., Gabriellan A.E., Garg N.S., Gelbart W.M., Classer K.,

Rad Rosine D., Helman T.J., Hernandez J.R., Houck J.,

Rad Alasko P., Lei Y., Karpen G. H., Ke Z., Kennison J.A., Kecchum K.A.,

Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Rak Liu X., Matush F., Karpen G. H., Wilskern D.R., Machland M., Nelson M., Murphy D., Lin X.,

Rak Liu X., Matush F., Rarpen G.H., Wilskern D.R., Parlur V., Resse M.G.,

Ray Alasko D.M., Pittman G.S., Pan S., Pollard J., Morbherfa F., Shen H.,

Rainer K., Spradling A.C., Stapleton M., Skupski M.P., Yao O.A.,

Ray Reinert K., Remington K., Shunkon M., Wang S., Wang S., Yao O.A.,

Ray Spier E., Spradling A.C., Stapleton M., Skupski M.P., Wang S., Wao O.A.,

Ray Stirkas R., Fector C., Turner R., Wang S., W
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; AE003800; AAF57713.1:
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Bukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE RNA POLYMERASE II SUBUNIT RPB10.
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Mismatches
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                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
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SEQUENCE 58 AA; 6561 MW; 4
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Best Local Similarity
                                                                                                                                                              SEQUENCE FROM N.A.
                                             Ephydroidea; Dro
NCBI_TaxID=7227;
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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                                                                                                                                               SEQUENCE FROM N.A.
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72 KKYCCS 77
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017778
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                 MEDLINE-21223349; PubMed-11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
EMBL. AF083031; AAK39726.1; -.
InterPro; IPPR000268; RNA_DOL_N.
Pfam; PF01194; RNA_DOL_N.
SEQUENCE 71 AA; 8391 MW; 7221827907FF5504 CRC64;
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Rhabditidae; Peloderinae; Caenorhabditis.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 11;
                                                                                                                                                                                                                                 Length 71;
                                                                                                                                                                                                                                                                           1; Indels
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X80821; CAA56787.1; -.
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SEQUENCE 150 AA; 18050 MW; 4E5E933C97FA075F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBOSOWAL PROTEIN L18A HOMOLOGUE (FRAGMENT)
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Last annotation update)
                                                                                                                                                                                                                               73.5%; Score 36; DB 8; 71.4%; Pred. No. 6.1;
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0; Mismatches
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75.0%;
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06,
19,
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01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
CD4.7 PROTEIN.
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Matches 5; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A.
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Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Escaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vera P.;
"A novel extracellular matrix protein from tomato plant associated with lignified secondary cell wall.";
Plant Cell 6:1035-1047(1994).
EMBL; X77373; CAA54561.1; --
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STRAIN=CV. RUTGENS BUDWED=7919979;
MEDLINE=950035699; Pubwed=7919979;
Domingo C., Gomez M.D., Canas L., Hernandez-Yago J., Conejero V.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
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Pred. No. 18;
1; Mismatches 0; Indels
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036694; AAB88345.1; -
SEQUENCE 263 AA; 29908 MW; 9551D43D09B7BACD CRC64;
                                                                                                                                                                                                            Du Z., Scheet P., "The sequence of C. elegans cosmid CD4.", Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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83.3%;
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26 88
88 AA; 9919 MW;
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 83.35,
5; Conservative
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Search completed: November 1, 2002, 14:49:53 Job time : 4.45338 secs
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       Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDIINE=21153246; PubMed=11231293;
Rahlfs S., Becker K.;
Thioredoxin peroxidases of the malarial parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5833;
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                                                                                                                                                                                         'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                         71.4%; Score 35; DB 5; Length 127;
83.3%; Pred. No. 15;
Live 1; Mismatches 0; Indels
                                                                                                                       Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018 (1598).
EMBL: 28157; CABO2915.1;
SEQUENCE 127 AA: 15008 MW; 6F015987A4E8446A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BA442A16.1 (EIA BINDING PROTEIN P300) (FRAGMENT).
EP300.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THIOREDOXIN PEROXIDASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                               216 AA
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EMBL; AF225978; AAK20024.1; -.
Peroxidase.
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MEDLINE*99069613; Pubmed=9851916;
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Best Local Similarity 83.3*
Thea 5; Conservative
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                                                                                            SEQUENCE FROM N.A.
F10D11.3 PROTEIN.
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51 QKYCC 55
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Q9BKL4
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                                                                                                                                                                      Blakey S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AL096765; CAB62921.1;
R InterPro; IPR001487; Bromodomain.
P Ffam; PF00439; bromodomain.1.
R PRINTS; PR00503; BROMODOMAIN.
R PROSITE; PS00633; BROMODOMAIN.
R PROSITE; PS0014; BROMODOMAIN.2; 1.
NON_TER 1 1 1
NON_TER 330 A3, 37707 MW; OIF502BCBFA7C751 CRC64;
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NCBI_TaxID=9606;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:41:32; Search time 0.411576 Seconds (without alignments) 752.611 Million cell updates/sec Run on:

US-09-606-129A-35 49 1 QKYCCSRK 8

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description .	P53004 homo sapien	075185 homo sapien	photo	013877 schizosacch	9046 methanococc	Q57649 methanococc	Q64302 mus musculu	_	Q99pe7 rattus norv			homo	mus m	12793 homo sapien			O9ptll gallus gall	homo	6	Q45412 ralstonia s	_	_			-	_		059298 pyrococcus		Q	_		P46021 escherichia
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001591 lycopersico P50701 solanum com P1470 nicotiana t P12670 lycopersico P50702 solanum com P50703 solanum com P5871 nicotiana t P34545 caenorhabdi P56633 conus purpu O26147 methanobact 098028 sulfolobus O9vc49 drosophila
TPM1_LYCES OS13_SOLCO OSMO_TOBAC OSMO_TOBAC OSM1_SOLCO OS13_SOLCO OS13_SOLCO OS13_SOLCO OS13_SOLCO CRP1_CAELC CXR7_COMPU RPON_METTH RPON_METTH RPON_SULLSO
238 246 246 247 250 251 251 251 66
67 . 3 . 3 . 6 . 7 . 3 . 3 . 6 . 7 . 3 . 3 . 6 . 7 . 3 . 3 . 6 . 5 . 3 . 3 . 6 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIA.
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 1; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable calcium-transporting ATPase KIAA0703 (EC 3.6.3.8).
KIAA0703.
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                ODFD3B386F4DFC0A CRC64;
                                                                                                                                                                                                                                        BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                               POLY VAL.
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
A -> T (IN REF. 2).
SD -> G (IN REF. 2).
D -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                              InterPro; IPR000683; GFO_IDH_MocA. Pfam; PF01408; GFO_IDH_MocA; 1. Oxidoreductase; NAD; NADP; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                    EMBL; AC005189; AAC25526.1; -. MIM; 109750; -.
                                                                                                                                                                                                                                                                                                                                                                  33488 MW;
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                        EMBL; X93086; CAA63635.1; -. EMBL; U34877; AAC35588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                     154
160
296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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289 QKYCCSRK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QKYCCSRK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATC4_HUMAN
075185;
                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
ATC4_HUMAN
                                                                                                                                                                                                                                      CHAIN
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P29741;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Putative APP-dependent helicase in ompH 5. region (ORFI) (Fragment).
Bacteria; Proteobacterium profundum (Photobacterium sp. (strain SS9)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   053 CYTOPLASMIC (BY SIMILARITY).
396 PHOSPHORYLATION (BY SIMILARITY).
695 MAGNESIUM (BY SIMILARITY).
696 MAGNESIUM (BY SIMILARITY).
349 SITE 2 (BY SIMILARITY).
350 SITE 2 (BY SIMILARITY).
354 SITE 2 (BY SIMILARITY).
354 SITE 2 (BY SIMILARITY).
354 SITE 2 (BY SIMILARITY).
355 SITE 2 (BY SIMILARITY).
368 SITE 2 (BY SIMILARITY).
378 SITE 2 (BY SIMILARITY).
379 SITE 2 (BY SIMILARITY).
379 SITE 2 (BY SIMILARITY).
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PROSITE; PS00154; ATPASE_E1_E2; 1.
Hydrolase; Calcium transport; Transmembrane; Phosphorylation; ATP-binding; Metal-binding; Magnesium; Calcium-binding;
                                                                                                                                                                                                                                          1 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
C (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
3 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
4 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                              5 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
6 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
7 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 39; DB 1; Length 963; 75.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                          8 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
9 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
                                                                                                                                                                                                                                  CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
           or send an email to license@isb-sib.ch)
                                                          Interpro; IPR004014; Cation_ATPase.
Interpro; IPR001757; E1-E2_ATPase.
Interpro; IPR001454; Hydrolase.
Interpro; IPR00661; Na_H_K_ATPase.
Pfam; PF00669; Cation_ATPase_C; I.
Pfam; PF00690; Cation_ATPase_N; I.
Pfam; PF00122; E1-E2_ATPase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                  EMBL; AB014603; BAA31678.1; -. HSSP; P04191; 1EUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                     Multigene family.
DOMAIN
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SEQUENCE FROM N.A
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947 EKYCCSPK 954
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NCBI_TaxID=74109;
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TRANSMEM
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DOMAIN
TRANSMEM
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SEQUENCE
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TRANSMEM
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CA_BIND
CA_BIND
CA_BIND
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CA_BIND
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YOM1_PHOPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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DEFICER 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOP1_METJA
Q59046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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TOP1_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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  qq
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                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
          Bartlett D.H., Chi E., Wright M.E., Sequence of the ompH gene from the deep-sea bacterium Photobacterium Seguence of the OmpH gene from the deep-sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           Shpakovskii G.V., Lebedenko E.N.;
"Three regions of Rpb10 mini-subunit of nuclear RNA polymerases are
strictly conserved in all eukaryotes (letter).";
Bloorg. Khim. 22:938-940(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shpakovskii G.V., Proshkin S.A., Lebedenko E.N.;
"Exon-intron organization rpb10+ and rpc10+ genes of
Schizosaccharomyces pombe, coding for mini-subunits of nuclear RNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       013877; 014458;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerases I, II, and III 8.3 kDa polypeptide
(EC 2.7.7.6) (ABC10-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.6%; Score 38; DB 1; Length 151; 62.5%; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S23215; S23215.
Hypothetical protein; Hydrolase; Helicase; ATP-binding;
DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 151
151 AA; 17086 MW; FC8FA7862EAC1805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Biol. (Mosk) 32:285-290(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
MEDLINE-97177445; PubMed=9054344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98271918; PubMed-9608944;
                                                                                                                  SIMILARITY TO DING.
MEDLINE-93219138; PubMed-8385320;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X67094; CAA47468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                         Gene 131:125-128(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 QRYCCNHK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase I-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QKYCCSRK 8
                                                                                                                                                        Koonin E.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPBX_SCHPO
013877; 014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDEWT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                         POLYMERASES.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
MISCELLANDROUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  III FOR 5S AND TRNA GENES.
-!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10 RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                            {RNA}(N).
-!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 15
DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS SHARED BY ALL 3 YEAST RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA topolsomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
(Untwisting enzyme) (Swivelase).
                                                                                                                                        SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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EMBL; AF027818; AAC16895.1; -.
EMBL; D89596; BAA22805.1; -.
EMBL; D89596; BAA22805.1; -.
EMBL; 298598; CAB11246.1; -.
HSSP; C26147; 1EF4.
Interpro; 1PR000268; RNA_DOl_N.
Fransferase; DNA-directed RNA Polymerase; Transcription;
Transferase; DNA-directed RNA Polymerase; Transcription;
Nuclear protein; Zinc; Metal-binding.
METAL 10 10 ZINC (BY SIMILARITY).
METAL 44 44 ZINC (BY SIMILARITY).
EMETAL 45 45 ZINC (BY SIMILARITY).
SEQUENCE 71 AA; 8276 MW; 8B9EEE8FD59A2458 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 71; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococcales; Methanococcaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                            entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                       -i. CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
-i. MISCELLANGOUS: WHEN A TOPOLOSOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
-i. SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOLSOMERASE FAMILY.
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utcrback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                               -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3.
DNA CLEAVAGE (BY SIMILARITY).
2F9C95753E202D82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
15-DEC-1996 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase subunit N (EC 2.77.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; DB 1;
No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003601; DNAtopl_ATP_bind.
InterPro; IPR003602; DNAtopl_DNA_bind.
InterPro; IPR000380; Pro_topoisomerase.
InterPro; IPR000380; Pro_topoisomerase.
InterPro; IPR002936; Toprim.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01131; Topoisom, 3.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00433; TOPIAC; 1.
SMART; SM00433; TOPIAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87832 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67605; AAB99673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%;
71.4%;
                                                                                                                   Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPON OR MJ0196.
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721
315
761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 KYCCGRE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KYCCSRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus.
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ACT_SITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-96337999; PubMed=8688087;

MEDLINE-96337999; PubMed=8688087;

But C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Button G.G., Blake J.A., FirzGerald L.M., Clayton R.A., Gocayne J.D.,

Rerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Rerlavage A.R., Mirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

T "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10 RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transmembrane 4 superfamily, member 1 (Tumor-associated antigen L6)
TMAST OR M3S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000268; RNA_pol_N.
Pfam; PF01194; RNA_pol_N; 1.
PROSITE; PS01112; RNA_POL_N_BKD; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 1; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND TOPOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E716EA406D65B831 CRC64;
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SIMILARITY).
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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ZINC
ZINC
ZINC
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71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67475; AAB98176.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AA; 8695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {RNA}(N)
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Q64302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Rattus norvegicus (Rat).
                                                                                                                                                                                  SUBFAMILY.
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TRANSMEM
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TRANSMEM
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG5_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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ABG5_RAT
        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Marken J.S., Bajorath J., Edwards C.P., Farr A.G., Schieven G.L., Hellstroem I., Hellstroem K.E., Aruffo A.; Membrane topology of the L6 antigen and identification of the protein epitope recognized by the L6 monoclonal antibody."; J. Biol. Chem. 269:7397-7401(1994).
                                                   J. BLOI. CORM. 203://39//40411374).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND LUNG. MODERATELY EXPRESSED IN LYMPH NODES AND KIDNEYS. ALSO PRESENT IN THYMIC
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20578753; PubMed-11138003;
Lee M.-H., Lu K., Hazard S., Yu H., Shulenin S., Hidaka H., Kojima
Allikmets R., Sakuma N., Pegoraro R., Srivastava A.K., Salen G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinge; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dean M., Patel S.B.; "Identification of a gene, ABCG5, important in the regulation of dietary cholesterol absorption."; Nat. Genet. 27:79-83(2001).
                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
93838E707D85FF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY, AND INDUCTION.
MEDLINE-20553648; Pubmed-11099417;
Berge K.E., Tian H., Graf G.A., Yu L., Grishin N.V., Schultz J.,
Kwiterovich P., Shan B., Barnes R., Hobbs H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                       STROWA AND FIBROBLASTS.
SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 5 (Sterolin-1).
                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 202;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                             EXTRACELLULAR (PROBABLE).
PROBABLE.
                                                                                                                                                                                                                                                                                  EXTRACELLULAR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                   22243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                       71.48;
83.38;
                                                                                                                                                                                                                EMBL; L15443; AAA39403.1; -.
                                                                                                                                                                                                                           EMBL; L15429; AAA17873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                     MGD; MGI:104678; Tm4sfl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                             115
162
183
129
142
202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 YCCSRQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YCCSRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG5_MOUSE
099PE8;
                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                    -i- SUBUNIT: May form heterodimers with ABCG8 or be tightly coupled to ABCG8 along a pathway regulating diatery-sterol absorption and excretion (By similarity).
-i- SUBCELLUIAR LOCATION: Integral membrane protein (Probable).
-i- TISSUE SPECIFICITY: Expressed in the intestine and, at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                         -!- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                                                    "Accumulation of dietary cholesterol in sitosterolemia caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
ATP-binding cassette, sub-family G, member 5 (Sterolin-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 35; DB 1; Length 652;
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CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLUIAR (POTENTIAL).
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80CE37ADCC19771E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Glycoprotein; Transmembrane; Transport.

DOMAIN 1 385 CYTOPLASMIC (POTENTIAL).

TRANSMEM 386 406 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prec. ...
                       mutations in adjacent ABC transporters."; Science 290:1771-1775(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1351659; Abog5.
InterPro: IPR003593; AAA.
InterPro: IPR003593; AAA.
InterPro: IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
PRO317E; SMO0382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF312713; AAG53097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73244 MW;
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                                                                                                                                                  liver into bile.
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585
592
652 AA;
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464
505
526
530
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569 QKYCC 573
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MEDINE-88211561; PubMed-3284746;
Stillman D.J., Bankler A.T., Seddon A., Groenhout E.G., Nasmyth K.A.
"Characterization of a transcription factor involved in mother cell
specific transcription of the yeast HO gene.";
                                                                                                                                                                                                                                                                                                                                       Nagai K., Nakaseko Y., Nasmyth K.A., Rhodes D.;
"Zinor-finger motifs expressed in E. coli and folded in vitro direct
specific binding to DNA.";
Nature 332:284-286(1988).
                                                                                                                                                                                                                                              Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Moll T., Tebb G., Surana U., Robitsch H., Nasmyth K.; Tebb G., Surana U., Robitsch H., Nasmyth K.; The role of phosphorylation and the CDC28 protein kinase in cell cycle-regulated nuclear import of the S. cerevisiae transcription
                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, MUTAGENESIS, AND INTRACELLULAR LOCALIZATION
                                                                                                                                                                                                                                                                                  Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces.
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                           MEDLINE=88156968; PubMed=2831463;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91347374; PubMed=1652372;
               Transcriptional factor SWI5.
SWI5 OR YDR146C OR YD8358.03C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 540-608
                                                                                                                                                                                            EMBO J. 7:485-494 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 66:743-758(1991).
                                                                                                                                                                                                                                     STRAIN-S288C / AB972;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actor SWI5.
                                                                                                                                                                                                                                                                                                               DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>-
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                                                                      STRAIN=Sprague-Dawley; TISSUE=Small intestine;
MEDLINE=20578753; PubMed=11138003;
Lee M.-H., Lu K., Hazard S., Yu H., Shulenin S., Hidaka H., Kojima H.,
Allikmets R., Sakuma N., Pegoraro R., Srivastava A.K., Salen G.,
Dean M., Patel S.B.;
"Identification of a gene, ABCGS, important in the regulation of
dietary cholesterol absorption.";
                                                                                                                                                                                                                                                      coupled to
               Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Rattus.
                                                                                                                                                                           Nat. Genet. 27:79-83(2001).
-!- FUNCTION: Transporter that appears to play an indispensable role in the selective transport of the dietary cholesterol in and out of the enterocytes and in the selective sterol excretion by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein (Probable). SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
                                                                                                                                                                                                                                                 SUBUNIT: May form heterodimers with ABCG8 or be tightly coupled ABCG8 along a pathway regulating diatery-sterol absorption and excretion (By similarity).
 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Glycoprotein; Transmembrane; Transport. DOMAIN 1 385 CYTOPLASMIC (POTENTIAL).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFGM; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
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 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                          SEQUENCE FROM N.A.
                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                            SUBFAMILY
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TRANSMEM
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CARBOHYD
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE CELL CYCLE-DEPENDENT PHOSPHORYLATION OF THREE SERINE RESIDUES PERVEYES SWIS FROM ENTERING THE NUCLEUS, AND IT ACCUMULATES IN THE CYTOPLASM. AS A CONSEQUENCE OF CDC28 KINASE INACTIVATION AT THE END OF ANAPHASE, THE THREE SERINE RESIDUES ARE DEPHOSPHORYLATED AND SWIS ENTERS THE NUCLEUS TO ACTIVATE TRANSCRIPTION. IT IS THEN RAPIDLY DEGRADED. THERONINE PHOSPHORYLATION ALSO SEEMS TO OCCUR. SIMILARITY: STRONG, TO YEAST METALLOTHIONEIN EXPRESSION ACTIVATOR
MEDLINE—93085741; PubMed=1433468;
Neuhaus D., Nakaseko Y., Schwabe J.W.R., Klug A.;
Isolution structures of two zinc-finger domains from SWIS obtained
zinc-finger structure with a third strand of beta-sheet.";
J. Mol. Biol. 228:637-651(1992).
J. Mol. Biol. 228:637-551(1992).
J. Mol. Biol. 228:637-551(1992).
J. PUNCTION: DETERMINES THE MOTHER-CELL-SPECIFIC TRANSCRIPTION OF THE
MATING-TYPE SWITCHING IN YEAST. RECOGNIZES A SPECIFIC SCORDENCE IN
THE PROMOTER OF THE HO GENE. ACTIVATES EGTZ TRANSCRIPTION IN A
CONCENTRATION-DEPENDENT MANNER. SYNTHESIZED DURING G2 AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR IN G1, BUT CYTOPLASMIC IN S, G2, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Swiss Institute of Bioinformatics and the
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PIR; S00342; TWBYS5. PDB; 1NCS; 10-JUL-96 PDB; 1ZFD; 14-OCT-96.

709 AA

PRT;

STANDARD

SWIS_YEAST
ID SWIS_YEAST
AC P08153;

RESULT 10

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1 OKYCC

Last sequence update)

01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequ

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us-09-606-129a-35.rsp

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P300_HUMAN
Q09472;
                                                                                     Query Match
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                                                                                                         Matches
                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   <u>;</u>
                                                                                                                                                                                   PHOSPHORYLATION (BY CDC28).
PHOSPHORYLATION (BY CDC28).
PHOSPHORYLATION (BY CDC28).
S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN ASSOCIATED WITH A-646 AND A-664.
S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN ASSOCIATED WITH A-522 AND A-664.
ASSOCIATED WITH A-522 AND A-644.
ASSOCIATED WITH A-522 AND A-644.
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEAR TARGETING SIGNAL (POTENTIAL).
                                   Pfam; PF02178; AT_hook; 1.
Pfam; PF00196; zf-C2H2; 3.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00384; AT_hook; 1.
SWART; SM00385; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Transcription regulation; Activator; Zinc-finger; DNA-binding; Repeat; Metal-binding; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                               71.4%; Score 35; DB 1; Length 709; 75.0%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 94.9 kDa protein C22E12.11C in chromosome I.
                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                            BEF5ED5BFB6E30F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         859 AA
                                                                                                                                                                                                                                                                                                         Pred. No. 66;
0; Mismatches
                                                                                                                                     ZINC FINGERS
                                                                                                                                               C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                   C2H2-TYPE
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         SGD; S0002553; SWI5.
InterPro; IPR000637; AT_hook.
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                            79775 MW;
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InterPro; IPR001965; PHD.
InterPro; IPR001214; SET.
                                                                                                                                                                                                                                                                                                                   6; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                    632
574
604
632
659
522
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NCBI_TaxID-4896;
TRANSFAC; T00776; -
                                                                                                                                                                                                                                                                           709 AA;
                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       269 QKYCLQRK 276
                                                                                                                                                                                                                                                                                                                                    1 QKYCCSRK 8
                                                                                                                                                                                                                                     646
                                                                                                                                                                                                                                                         664
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                                                                                                                           3D-structure
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Q10362;
                                                                                                                                                                                                                                                                            SEQUENCE
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ZN_FING
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SITE
                                                                                                                                                                                               MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE—95011587; PubMed=7523245;
MEDLINE—95011587; PubMed=7523245;
ECKNET R., EWEND M.E., Newsome D., Gerdes M., Decaprio J.A.,
Lawrence J.B., Livingston D.M.;
"Molecular cloning and functional analysis of the adenovirus ElA-
associated 300-kD protein (p300) reveals a protein with properties of
a transcriptional adaptor.";
Genes Dev. 8 869-884(1994).
-:- FUNCTION: PROBABLE TRANSCRIPTIONAL ADAPTOR REQUIRED FOR THE
ACTIVITY OF CERTAIN COMPLEX TRANSCRIPTIONAL REGULATORY ELEMENTS.
MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO AND MAY BE
INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS ELA
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                  Length 859;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                       PROSITE; PS50280; SET; 1.
Hypothetical protein; Zinc-finger.
226 341 SET.
SEQUENCE 859 AA; 94886 MW; B4865BF40FD2C5D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                               Score 35; DB 1;
Pred. No. 77;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
EP300 OR P300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2414 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001487; Bromodomain.
InterPro; IPR003101; KIX.
InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; ZnF_ZZ.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00772; KX; 1.
                                                                                                                                                                                                                                                                                  71.4%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00249; PHD; 1.
SMART; SMO0317; SET; 1.
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                                                                                                                                                                                                                                                                                                            Best Local Similarity
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221 KFCCSR 226
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SMART; SM00291; ZnF_ZZ; 1
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                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phosphorylated CREB binds specifically to the nuclear protein CBP.";
Nature 365:855-859(1993).
-!- FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO
PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AUGMENTS
THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF
                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                              Gaps
PROSITE; PS01357; ZF_ZZ_1; 1.
PROSITE; PS50135; ZF_ZZ_2; 1.
Transcription regulation; Nuclear protein; Bromodomain; Cell cycle; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94019866; Pubwed-8413673;
Chrivia J.C., Kwok R.P.S., Lamb N., Hagiwara M., Montminy M.R.,
Goodman R.H.;
                                                                      BINDING REGION FOR ELA ADENOVIRUS.
ZZ-TYPE.
POLY-SER.
POLY-GLU.
                                                                                                                                                                             ;
                                                                                                                                                        Score 35; DB 1; Length 2414; Pred. No. 1.7e+02;
                                                                                                                                                                             1; Indels
                                                                                                                                     6BFF909EE4B9D693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMP-RESPONSIVE GENES.
-- SUBCELLULAR LOCATION: NUClear.
-- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                         PRT; 2441 AA
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                           POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T01318; -...
MGD; MGI:1098280; Crebbp.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001019; TAZ_finger.
InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; ZnF_ZZ.
Pfam; PF00439; bromodomain; 1.
Pfam; PF02172; KIX; 1.
Pfam; PF02135; Zf-TAZ; 2.
                                                       572 1139
54 1707
7 1826
7 1526
2195
8, 264143 M
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                                                                                                                                                        71.4%;
83.3%;
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                          CREB-binding protein. CREBBP OR CBP.
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                    2414 AA;
                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                       1572
1664
797
1519
2066
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                                                            DOMAIN
DOMAIN
ZN_FING
                                                                                                                                    SEQUENCE
                                                                                                     DOMAIN
DOMAIN
                                                    DOMAIN
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                                                                                                                           DOMAIN
                                                                                                                                                                            Matches
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CBP_MOUSE
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-i- FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AGGMENTS THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF CAMP-RESPONSIVE GENES.
-i- SUBUNIT: INTERACTS WITH SMADI, SMAD2. AND SMAD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeleznik-Le N.J.;
"MLL is fused to CBP, a histone acetyltransferase, in therapy-related acute myeloid leukemia with a t(11:16)(q23:pJ3.3).";
Proc. Natl. Acad. Sci. U.S.A. 94:8732-8737(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97321049; PubMed=9177780; Giles R.H., Petrij F., Dauwerse H.G., den Hollander A.I., Lushnikova T., van Ommen G.J.B., Goodman R.H., Deaven L.L., Doggett N.A., Peters D.J.M., Breuning M.H.; "Construction of a 1.2-Mb contig surrounding, and molecular analysis of, the human CREB-binding protein (CBP/CREBBP) gene on chromosome 16p13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrow J., Stanton V.P., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; "The translocation t(8:16)(pl1:pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).
                          PROSITE; PS50014; BROMODOMAIN_2; 1.
PROSITE; PS61357; ZF_ZZ_1; 1.
PROSITE; PS50135; ZF_ZZ_2; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                      265474 MW; OABB028C3112F419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; I
Pred. No. 1.7e+02;
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15-JUL-1998 (Rel. 36, Oreated)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2442 AA
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                                                                                                                                               BROMODOMAIN
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POLY-PRO.
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POLY-GLU.
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PROSITE; PS00633; BROMODOMAIN_1; 1. PROSITE; PS50014; BROMODOMAIN_2; 1.
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MEDLINE=97385172; PubMed=9238046;
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MEDLINE=96376968; Pubmed=8782817;
                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
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1065
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1949
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2216
2299
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                                                                                                                                                                                                                                                         1968 19
2082 20
2200 22
2296 22
241 AA;
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Best Local Similarity
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1062
1556
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                                                                                                                         Zinc-finger
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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TXOF_HADVE
P81599;
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                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           DISEASE: INVOIVED IN ACUTE LEUKEMIAS BY CHROMOSOMAL TRANSLOCATIONS T(8:16)(P11;P13) INVOLVING CBP AND MOZ, AND T(11;16)(Q23;P13.3) INVOLVING CBP AND MLL.

INVOLVING CBP AND MLL.

SINDROME (RTS), A DISORDER CHARACTERIZED BY CRANIOFACIAL ABNORMALITIES, BROAD THUMBS, BROAD BIG TOES, MENTAL RETARDATION AND A PROPENSITY FOR DEVELOPMENTOF MALIGNANCIES.

SIMILARITY: CONTAINS 1 BROMODOMAIN.

SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                     | MIM; 600140; -... | MIM; 6001019; TAZ_finger. | InterPro; IPR000191; TAZ_finger. | InterPro; IPR000191; TAZ_finger. | InterPro; IPR000191; ZnF_ZZ. | MIM; PF02135; Zf-TAZ; 2... | MIM; PF02135; Zf-TAZ; 2... | MIM; PF001503; BROWDOMAIN. | MIM; PRINTS; PR00503; BROWDOMAIN. | MIM; SWART; SW00291; ZnF_ZZ; 1... | MIM; PR051TE; PS00143; ZF_ZZ_1: | MIM; PR051TE; PS00143; ZF_ZZ_2: | MIM; PR051TE; PS0135; ZF_ZZ_2: | MIM
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0
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42D084619475F3D2 CRC64;
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-> F (IN REF. 2).
-> P (IN REF. 2).
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CREB-BINDING.
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CYS/HIS-RICH.
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POLY-GLU.
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POLY-GLN.
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POLY-GLN.
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POLY-GLN.
SUBCELLULAR LOCATION: Nuclear.
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83.3%;
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Matches 5; Conserv
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DOMAIN
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3 YCCSRK 8 ||| || 1198 YCCGRK 1203

g S RESULT 15 TXOF_HADVE

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Gaps
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Eur. J. Biochem. 264.488-494(1999).

-i- FUNCTION: INHIBITS INSECT, BUT NOT MAMMALIAN, VOLTAGE-GATED
                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Chellcerata; Arachnida; Araneae;
Mygalomorphae; Hexathelldae; Hadronyche.
NCBL_TaxID=6904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                              Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99421654; PubMed-10491095;
Wang X.-H., Smith R., Fletcher J.I., Wilson H., Wood C.J.,
Merlin E.H., King G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCIUM CHANNEL CURRENTS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by the venomous gland HSSP; P56207; LAXH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium channel inhibitor; Toxin; Neurotoxin.
DISULEID 1 2 BY SIMILARITY.
DISULEID 17 36 BY SIMILARITY.
SEQUENCE 37 AA; 3951 MW; EECIGAEG7EE3F36A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 34; DB 1;
100.0%; Pred. No. 9.7;
Live 0; Mismatches (
                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Omega-atracotoxin-Hvlf (Omega-AcTx-Hvlf)
37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 1, 2002, 14:47:51
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 2.41158 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 KYCCS 19
                                                                                                                                                                                                                                                                                                                                                     FISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KYCCS 6
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us-09-606-129a-35.rpr

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 1, 2002, 14:43:58; search time 0.848875 Seconds (without alignments) 905.569 Million cell updates/sec Run on:

US-09-606-129A-35 49 1 QKYCCSRK 8

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	biliverdin reducta	biliverdin reducta	hypothetical prote	u	hypothetical prote	DNA-directed RNA p	Putative RNA polym	ribosomal protein	hypothetical prote	Ψ	DNA-directed RNA p	glycine-rich prote	hypothetical prote	L6 antigen - mouse	osmotin - common t	hypothetical prote	_	hypothetical prote	hypothetical prote		transcription adap	transcription coac	CREB-binding prote		allergen Ra5G prec	probable membrane	protein from bacte	exopolysaccharide	hypothetical prote
		1 1 1 1 1 1																												
ı	ID	G02066	S62624	S23215	B82148	T27220	T43545	C90129	S47354	T32530	B64506	E64324	T07013	T20707	A53399	S34794	T33038	TWBYS5	T38168	T23094	T23095	A54277	839162	S39161	T13828	ARRA5G	S69304	E97101	S	C86336
	DB	7	~	~	~	~	ď	~	~	7	7	7	ď	~	~	7	7	Н	N	7	~	7	~	ď	7	-	a	~	7	7
	Length	296	296	151	703	571	71	7.1	150	263	761	9/	88	127	202	243	385	709	859	959	961	2414	2440	2441	3190	73	129	236	418	485
æ	Query Match	100.0	100.0	77.6	77.6	75.5	•	73.5	•	•		71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	69.4	4.69	69.4	69.4	69.4
	Score	49	49	38	38	37	36	36	36		36		35	35	35	35	35	35	35	35	35	32	35	32	32	34	34	34	34	34
	Result No.	1	7	e	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	hypothetical prote	genome polyprotein	genome polyprotein	hypothetical prote	alpha-2-macroglobu	DNA-directed RNA p	DNA-directed RNA p	ribosomal protein	probable DNA-direc	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	hypothetical prote	pathogenesis-relat
S31126	T29275	A44212	MNWWHE	T03884	A53102	A75172	A69391	S38604	H71042	T47958	S56953	A65112	F91139	A85985	S31829
7	7	П	г	7	Н	7	N	Н	7	CI	7	7	7	7	7
503	1484	1691	1693	2025	4543	9	16	86	119	129	183	210	210	210	233
9.4	9.4	9.4	9.4	.4.69	9.4	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3
ø	9	9	9	9	9	9	9	9	9	9	9	ø	φ	9	Q
34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	4.5

## ALIGNMENTS

Diliverdin reductase (EC 1.3.1.24) - human N:Alternate names: biliverdin IX-alpha reductase C;Species: Homo sapiens (man) C;Dete: 21-Dec. 1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998 C;Detes 21-Dec. 1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998 C;Detes 21.0
lternate names: biliverdin IX-alpha reductase Specias: Homo sapiens (man) Specias: Homo sapiens (man) Ate: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change Accession: G02066 Accession: G02066 Amitted to the EMBL Data Library, August 1995 Accession: G02066 Accession: G0206 Accession: G02
っ マックマンググダイスをかいと つめて

Diliverdin reductase (EC 1.3.1.24) - human
N:Alternate names: biliverdin IX-alpha reductase
C:Species: Homo sapiens (man)
C:Species: Boot-1996 **sequence_revision 09-May-1997 **text_change 21-Jul-2000
C:Date: 28-Oct-1996 **sequence_revision 09-May-1997 **text_change 21-Jul-2000
C:Accession: 562624; 562622; 529736
R:Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Bur. J. Biochem. 235, 372-381, 1996
A:Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A:Reference number: 562622; MuID:96202961
A:Accession: 562624

A. Molecule type: MRNA A; Residues: 1-296 <MAI> A; Cross-references: EMBL:X93086; NID:91246748; PIDN:CAA63635.1; PID:91246749 A; Accession: S6262 A; Molecule type: protein A; Residues: 3-24, "X', 26-27, "X', 29-36;48-74;228-234;235-248 <MAF> R; Maines, M.D.: Trakshel, G.M. Arch. Biochem. Biophys. 300, 320-326, 1993 A; Title: Purification and characterization of human biliverdin reductase. A; Reference number: S29736; MUID:93143333

A; Molecule type: protein A;Residues: 3-24,'X',26-27,'X',29-36;48-74;228-234;235-248 <MAW> A;Note: the sequence of peptide 1 from page 323 seems not to belong to this protein

Gaps

```
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-71 < MUR>
A; Cross references: EMBL:298598; PIDN:CAB11246.1; GSPDB:GN00066; SPDB:SPAC1B3.12c
A; Cross references: EMBL:298598; PIDN:CAB11246.1; GSPDB:GN00066; SPDB:SPAC1B3.12c
A; Experimental source: strain 972h-; cosmid c1B3
B; Sakurai, H.; Ishihama, A.
Gene 196, 165-174, 1997
A; Title: Gene organization and protein sequence of the small subunits of Schizosaccha
A; Reference number: 225897; MUID:97464063
A; Reference number: 225897; MUID:97464063
A; Reference number: 225897; MulD:97464063
A; Reference number: 225897; MulD:97464063
A; Reference number: 225897; MulD:97464063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-directed RNA polymerase (EC 2.7.7.6) II chain Rpb10 - fission yeast (Schizosaccha
                                                                                                                                                                                                                                                 A; Residues: 1-571 <WIL>
A; Residues: 1-571 <WIL>
A; Cross-references: EMBL: Z99281; PIDN: CAB16509.1; GSPDB: GN00022; CESP: Y57G11C.7
A; Experimental source: clone Y57G11C
C; Genetics:
A; Gene: CESP: Y57G11C.7
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27220
S;McMurray, A.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 03-Nov-2000
C;Accession: T43545; T38031; T52005
R;Shpakovski, G.V.; Lebedenko, E.N.; Proshkin, S.A.
submitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T43545
A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-71 <SHP>
A;Cross-references: EMBL:AF027818; PIDN:AAC16895.1
A;Experimental source: strain 972(-)
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1997
A;Reference number: Z21763
A;Reference number: Z21763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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A;Note: rpb10
C;Superfamily: DNA-directed RNA polymerase II chain RPB10
C;Keywords: nucleotidyltransferase; transcription
                                                                                                                                      A;Reference number: 220330
A;Accession: T27220
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2;
Pred. No. 36;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-71 - SSAK>
A;Cross-references: EMBL:D89596; PIDN:BAA22805.1
A;Experimental source: strain JY741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
A; Introns: 72/2; 155/3; 214/1; 249/3; 279/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.5
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 71.4 Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z22564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||| |:
192 RKYCCPRR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QKYCCSRK 8
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*Residues: 1-703 <HBID.
A;Cross-references: GB:AE004261; GB:AE003852; NID:99656382; PIDN:AAF95003.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Photobacterium sp.
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
C; Accession: 523215
R; Bartlett, D.H.; Chi, E.; Wright, M.E.
S; Danitted to the EMBL Data Library, June 1992
A; Description: Nucleotide sequence of the OMPH gene and construction of an OMPH mutant A; Reference number: 523213
A; Accession: 523215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-dependent helicase, DinG family VC1855 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae (strain 20-Aug-2000 #text_change 02-Feb-2001 C;Apecission: B8-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Apocession: B82148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
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A;Molecule type: DNA
A;Residues: 1-151 <BAR>
A;Cross-references: EMBL:X67094; NID:g45887; PIDN:CAA47468.1; PID:g45890
                                                   C; Reywords: oxidoreductase F;3-296/Product: biliverdin reductase IX-alpha #status experimental
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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0
                                                                                                                                         100.0%; Score 49; DB 2; Length 296
100.0%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.6%; Score 38; DB 2; Length 151; llarity 62.5%; Pred. No. 28; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 703;
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Nypothetical protein Y57G11C.7 - Caenorhabditis elegans
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein 1 · Photobacterium sp.
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62.58;
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Best Local Similarity 62.5%,
                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
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289 QKYCCSRK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||: |
119 QRYCCNHK 126
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| 131 QRYCCSER 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                      1 QKYCCSRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QKYCCSRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: B82148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
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     C;Genetics:
A;Gene: BVR
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ö

Gaps

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A; Experimental source: strain Bristol N2; clone CD4
                                                                  A;Gene: CESP:CD4.7
A;Map position: 4
A;Introns: 121/3; 156/1; 243/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Start codon: GTG
C,Superfamily: DNA top
C,Keywords: isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 KYCCGRE 131
                                                                                                                                                                                                                                                                                                                                                                                                                       1111:1
234 KYCCTR 239
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                                                                                                                                                                                                                                                                                                                                                                        2 KYCCSR 7
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                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
B64506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                   Rei
                                                                                                                                                                                                                                              G:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-Nay-2001 #sequence_revision 10-Nay-2001 #text_change 24-May-2001
C:Date: 10-Nay-2001 #sequence_revision 10-Nay-2001 #text_change 24-May-2001
C:Date: 10-Nay-2001
B:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; F.
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671
A:Reference number: A99082; MUID:11323671
A:Reference number: A99082; MUID:11323671
A:Reference number: A99082; MUID:11323671
C:Caos-references: GB:AF083031; NID:g13794349; PIDN:AAK39726.1; GSPDB:GN00152
C:Genetics:
                                                                                                                                                                                                                       Putative RNA polymerase II subunit Rpb10 [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T3259
R;Du, Z.; Scheet, P.
Submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid CD4.
A;Reference number: 221185
A;Accession: T32530
A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 24-Oct-1997 #text_change 05-Nov-1999
C;Accession: S47354
R;Zenz, K.I.
R;Zenz, K.I.
A;Reference number: S47353
A;Reference number: S47353
A;Reference number: S47353
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A;Residues: 1-150 <2EN>
A;Cross-references: EMBL:X80821; NID:9527579; PIDN:CAA56787.1; PID:9527580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 36;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 150
Pred. No. 57;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosomal protein L18a homolog - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 73.5%;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: nucleomorph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genome: nucleomorph
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1:111 |
QRYCCRR 47
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S47354
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DNA topoisomerase (EC 5.99.1.2) - Methanococcus jannaschii
N;Alternate names: topoisomerase I
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #text_change 21-Jul-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: B64506
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Rikhess, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Methanococcus januaschii
C:Date: 13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change 23.Apr-1999
C:Accession: E64324
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bolt, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A;Reference number: A64300; MUID:96337999
A;Reference number: A64300; MUID:96337999
A;Ression: E64324
A;Reletence number: A64300; MUID:963400; Muid:Accession: E64024
A;Reletence number: A64300; MUID:963400; Muid:Accession: E64024
A;Reletence number: A64300; Muid:Accession: Accession: Accession:
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                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Length 263;
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Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                        0; Indels
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C;Superfamily: DNA-directed RNA polymerase II chain RPB10
C;Keywords: nucleotidyltransferase; transcription
      ;;
      DB
81;
                                                                                                                  1; Mismatches
      Score 36;
Pred. No.
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Query Match 73.5%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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us-09-606-129a-35.rpr

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Gaps

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5;

Score 35; DB Pred. No. 99; 1; Mismatches

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R; Marken, J.S.; Bajorath, J.; Edwards, C.P.; Farr, A.G.; Schieven, G.L.; Hellstroem, J. Biol. Chem. 269, 7397-7401, 1994
A; Title: Membrane topology of the L6 antigen and identification of the protein epitop A; Reference number: A53399; MUID:94171760
A; Accession: A53399
A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Nicotiana tabacum (common tobacco)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S34794; S37294
R;Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
Plant Physiol. 90, 1096-1101, 1989
A;Title: Molecular cloning of osmotin and regulation of its expression by ABA and ada A;Reference number: S34794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: EMBL:M29279; NID:g170278; PIDN:AAA34089.1; PID:g170279 C;Superfamily: thaumatin I
                                                                                                                                                                                                          A; Cross-references: GB:L15429; NID:g468909; PIDN:AAA17873.1; PID:g476343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:M29279
R;Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
submitted to the EMBL Data Library, February 1990
A;Reference number: S37294
A;Accession: S37294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.4%; Score 35; DB 2; Le 50.0%; Pred. No. 1.1e+02; Live 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 1, 2002, 14:51:03 Job time : 3.01554 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128,'I',130-243 <SI2>
                                                                                                                                                                                                                                                                71.48;
83.38;
                                                                                                                                                                                                                                                                                        Local Similarity 83.3
nes 5; Conservative
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                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-202 <MAR>
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A;Molecule type: mRNA
A;Residues: 1-243 <SIN>
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                                                                                                                                                                                                                                                                          July and the protein precursor - tomato

Ni Alternate names: cell wall protein
C; Specias: Lycopersion esculentum (tomato)
C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C; Accession: T07013
R; Dominjoo, C; Gomez, M.D; Canas, L.; Hernandez-Yago, J; Conejero, V.; Vera, P.
Plant Cell 6, 1035-1047, 1994
A; Title: A novel extracellular matrix protein from tomato plant associated with lignifie
A; Reference number: 215861; MUID:95003699
A; Reference number: 215861; MUID:95003699
A; Residues: 1-88 comes
A; Residues: 1-88 comes
A; Residues: 1-88 comes
A; Residues: 1-88 comes
A; Cross-references: EMBL:X77373; NID:9541681; PIDN:CAA54561.1; PID:9541682
A; Cross-references: EMBL:X737373; NID:9541681; expanded laeves
F; 1-25/Domain: signal sequence #status predicted <MAT>
F; 26-88/Product: glycine-rich protein #status predicted <MAT>
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Cipacies: Caenorhabditis elegans
Cipacies: Caenorhabditis elegans
Cipacesion: T20707
Ribobson, R.
Submitted to the EMBL Data Library, October 1996
A; Reference number: 219312
A; Caession: T20707
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-127
A; Residues: 1-127
A; Residues: 1-127
A; Cross-references: EMBL: 281057; PIDN: CAB02915.1; GSPDB: GN00019; CESP: F10D11.3
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C;Species: Nus musculus (house mouse)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Nov-1999
C;Accession: A53399
                                                        Gaps
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DB 2; Length 76;
53;
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.58;
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83.3%; Pred. No. 58;
Live 1; Mismatches
                                                     1; Mismatches
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  Score 35;
Pred. No.
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A, Gene: CESP:F10D11.3
  71.48;
71.48;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                     Conservative
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A; Introns: 22/3; 52/3; 98/3
                     Best_Local Similarity
Matches 5; Conserv
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44 KKYCCRR 50
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118 FCCSRK 123
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     Query Match
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Length 243;

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KYCCSK
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292.168 Million cell updates/sec
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                                                                                                     November 1, 2002, 14:44:48; Search time 0.66881 Seconds
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Sequence 4,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-013-780-2
US-08-835-261A-4
US-08-839-711-4
US-08-227-536-2
PCT-US95-0468-2
US-08-194-468-2
US-08-961-739-2
US-08-961-739-2
US-08-961-739-2
US-08-965-9038-6
US-08-965-9038-6
US-08-840-316-1
US-08-840-316-1
US-08-478-507-7
US-08-478-507-7
US-08-471-971-1
PCT-US93-088499-1
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US-08-857-076-113
US-08-815-868A-7
US-08-495-819B-7
US-08-315-868A-7
US-08-315-868A-6
US-08-315-868A-6
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US-08-315-868A-6
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                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                    US-09-606-129A-35
                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Query
Match Length D
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93, Appli
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Sequence 41,
Sequence 42,
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Sequence 9
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ZIP: 20850-4373

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 94202667.6

FILING DATE: 12-SEP-1995

PRIOR APPLICATION NUMBER: EP 94202667.6

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: GORMLEY, MARY E.

REGISTRATION NUMBER: 34,409

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BUNSTEAD, Janene Marilyn J.M.
APPLICANT: TOMLEY, Fiona Margaret F.
APPLICANT: TOMLEY, Fiona Margaret F.
APPLICANT: DUNN. Patrick Paul James P.
APPLICANT: VERNEULEN, Arnoldus Nicolaas A.N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 2
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5885568el N.V
        US-08-857-076-40

US-08-857-076-41

US-08-857-076-42

US-08-657-076-42

US-08-619-936-1

US-08-463-989-9

US-08-003-574-9

US-08-003-574-9

US-08-486-099-93

US-08-486-099-93

US-08-486-099-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93

US-08-475-668A-93
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Pred. No. 43;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 PICCARD DRIVE #206 CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08527044 Patent No. 5885568 GENERAL INFORMATION:
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83.3%;
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amino acid
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
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71.4%; Score 35; DB 2; Length 202; 83.3%; Pred. No. 1e+02;
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Patent NO. 6033870
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, PULY:
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESTING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/839,711 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0298 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 5; Conservative
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STRANDEDNESS: single
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abbar 31/2
STREET: 31/2
TTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: GenBank
CLONE: 476343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-839-711-4
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                     Sequence 2, Application US/09013780
Patent No. 6001363
GENERAL INFORMATION:
APPLICANT: BUMSTEAD, Janene Marilyn J.M.
APPLICANT: TOMLEY, Flona Margaret F.
APPLICANT: VERBULEN, Arnoldus Nicolaas A.N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6001363el N.V
STREET: 1300 PICCARD DRIVE #206
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIATE: WOLVER TO STATE TO STAT
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APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 4
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,261A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Score 36; DE 83.3%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/013,780 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/527,044
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/0885261A Patent No. 5922566 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: GORMLEY, MARY E. REGISTRATION NUMBER: 34 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                             Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 KYCCSK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KYCCSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-855-261A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-013-780-2
US-09-013-780-2
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2414 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-227-536-2
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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STREET: Te..
TmV: Boston
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                                                              Score, 35; DB 3; Length 202; Pred. No. 1e+02; 0; Indels 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                        Sequence 4, Application US/09227224

Fatent No. 6350581

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: Neil C.
TITLE OF INVENTION: Neil C.
CORRESPONDENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,224
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APPLICATION NUMBER: 08/855,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION UNDBER: 36,749
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-08-227-536-2
; Sequence 2, Application US/08227536
; Patent No. 5658784
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                                                                 71.4%;
83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                              Query Match 71.4
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
; LIBRARY: GenBank
; CLONE: 476343
US-08-839-711-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LIBRARY: GenB:
; CLONE: 476343
US-09-227-224-4
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                                                                                                                                               192 YCCSRQ 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                              3 YCCSRK 8
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                                                                                                                                                                                                                              US-09-227-224-4
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APPLICANT: Eckner, Richard
APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9504682
GENERAL INFORMATION:
APPLICANT:
TITLE.OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
TITLE.OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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STREET: Ten Post Office Square
CITY: Boston
                                                                                                                                                                                               E: Weingarten, Schurgin, Gagnebin & Hayes
Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1;
Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DFCI-308XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFRX: (617) 542-2290
TELEFRX: (617) 542-2290
TELEFRX: (617) 542-2290
TELEFRX: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
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GENERAL INFORMATION:
APPLICANT: Montminy, Marc R.
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
CURRENT APPLICATION NUMBER: US/08/961,739A
GURRENT FILING DATE: 1997-10-31
EARLIER FILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 3; Length 2441;
Pred. No. 8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08965903B
Patent No. 6060275
GENERAL INFORMATION:
APPLICANT: Hacohen, Nir
APPLICANT: Krasnow, Mark A.
TITLE OF INVENTION: SPROUTY PROTEIN AND CODING
TITLE OF INVENTION: SEQUENCE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,903B
FLING DATE: 07-NOV-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Petithory, Joanne R
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0177.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-961-739-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030232
FILING DATE: 07-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
                                                                                               ; Sequence 2, Application US/08961739A
; Patent No. 6063583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.4
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650-324-0960
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||
| Db | 1199 YCCGRK 1204
1199 YCCGRK 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus
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                                                           RESULT 9
US-08-961-739-2
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APPLICANT: MOINTINDY, MATC R.
APPLICANT: MOINTINDY, MATC R.
ASSAYS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
TITLE OF INVENTION: RESPONSIVE GENES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
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                                                                                                                                                                                                                                                                                                                                                Score 35; DB 5; Length 2414; Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 2441;
                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 35; DB 1;
83.3%; Pred. No. 8e+02;
tive 0; Mismatches
                           ATORNEY AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
RECISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-308Xq999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEPHONE: (617) 542-2290
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2414 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9672
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)-546-4737
TELEPHONE: (619)-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08194468 Patent No. 5750336
14-April-1994
                                                                                                                                                                                                                                                                                                                                                  71.4%;
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.33
These 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein PCT-US95-04682-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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STATE: California
                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                     linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1162 YCCGRK 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YCCSRK 8
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                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-194-468-2
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GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Tasrev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Abernethy, Nevin
APPLICANT: Amble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000-1037c1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 34; DB 4; Length 174; 83.3%; Pred. No. 1.3e+02;
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NAME: Richard W. Bork
REGISTRATION NUMBER: 36.459
REFERENCE/DOCKET NUMBER: 2026-4255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
                                                                                                      RESULT 12
US-09-383-586-12
: Sequence 12, Application US/09383586
: Patent No. 6242419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08840316 Patent No. 6054567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity Bo...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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: USA
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                                          70 QSHCCSR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 YCCRRK 121
    1 QKYCCSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mouse US-09-383-586-12
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US-08-840-316-1
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                                                                                                                                                                                                                            69.4%; Score 34; DB 3; Length 117; 71.4%; Pred. No. 91; ive 1; Mismatches 1; Indels
                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein NOLECULE TYPE: protein SURGINAL SOURCE: INDIVIDAL ISOLATE: h-spryl cysteine-rich region US-08-965-903B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hacohen, Nir
APPLICANT: Krasnow, Mark A.
TITLE OF INVENTION: SPROUTY PROTEIN AND CODING
TITLE OF INVENTION: SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030232
FILING DATE: 07-NOV-1996
ATTORNEY AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0177;30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/965,903B
FILING DATE: 07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08965903B Patent No. 6060275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; INDIVIDUAL ISOLATE: h-spry1
US-08-965-903B-20
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
                     SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.48
Matches 5; Conservative
                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-324-0960
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US-08-965-903B-20
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Patent No. 6207416
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei. A., Emerson,
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 3; Length 1693;
Pred. No. 8.3e+02;
1; Mismatches 1; Indels
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REFERENCE/DOCKET NUMBER: 4600-0183.22 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2026-4032US4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING STEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA: D. APPLICATION NOTA: D. APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1693 AMINO ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                        TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.4%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-478-507-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN
                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
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US-08-809-523-1
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APPLICANT: Yarbough, Patrice O
APPLICANT: Yarbough, Patrice O
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Fram. Albert
APPLICANT: Tam, Albert
APPLICANT: Try, Kirk E
APPLICANT: Fry, Kirk E
APPLICANT: Fram. Albert
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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O
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILIG DATE: 07-JUN 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 34; DB 3; I
71.4%; Pred. No. 8.3e+02;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/20,921
FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 07/367,486
16-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
ATTORNEX/AGENT INFORMATION:
                                  TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08478507
Patent No. 6120988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                    UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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FILING DATE: 16-JUI
                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: UNKNOWN US-08-840-316-1
                                                                                                                                                                                                                                          TYPE: AMINO ACID STRANDEDNESS: UNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 QAFCCSR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-478-507-7
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0; 0; Gaps Matches 5; Conservative 1; Mismatches 1; Indels Search completed: November 1, 2002, 14:52:00 Job time: 2.66881 secs Qy 1 QKYCCSR 7 | :|||| Db 333 QAFCCSR 339

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us-09-606-129a-35.rag

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November 1, 2002, 14:40:53 ; Search time 1.8135 Seconds (without alignments) 489.985 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                               Sequence:
                                                                                                                      Run on:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa1981.DAT:*
3: /SIDS1/gcgdata/geneseq-emb1/Aa1981.DAT:*
4: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1981.DAT:*
5: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1981.DAT:*
6: /SIDS1/gcgdata/geneseq-emb1/Aa1985.DAT:*
6: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1985.DAT:*
7: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1986.DAT:*
8: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1988.DAT:*
9: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1989.DAT:*
10: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1989.DAT:*
11: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1990.DAT:*
12: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1991.DAT:*
13: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1991.DAT:*
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13: /SIDS1/gcgdata/geneseq-geneseqp-emb1/Aa1991.DAT:* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*/SIDSI/gcgdata/geneseqpe-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseqyeeneseqpe-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqpe-embl/AA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/geneseg/genesegp-embl/AA1994.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA1995.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA1996.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* .. 14: 15: 17: 19:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human secreted pro	Gene 34 human secr	Human secreted pro	Human colon cancer	Drosophila melanoq	T-lymphocyte stimu	Novel human diagno	Human myelin P0 pr	Chlamydia pneumoni	Nicotiana tabacum	Tobacco osmotin pr
SUMMARIES	ID	4	AAB44820	AAB44821	AAG74903	ABB69460	AAR84086	ABG27093	AAB99956	AAY34717	AAW69751	AAW94510
	DB	21	21	21	22	22	17	22	22	20	13	20
	Query Match Length DB	74	119	119	124	58	109	505	124	189	246	246
ap (	Query Match	79.6	79.6	79.6	9.62	73.5	73.5	73.5	71.4	71.4	71.4	71.4
	Score	39	39	39	39	36	36	36	35	35	35	35
	NO.	п	2	m	7	S	9	7	۵	σ	10	11

Komatsoulis G;

Rosen CA, Ruben SM, WPI; 2000-602355/57

Novel human diagno Fucalyprus grandis	Transcription fact	Cellular transcrip	CREB binding prote	Cellular transcrip	Mouse nuclear CREB	Mouse wound healin	Human wound healin	Amino acid sequenc	Drosophila melanog	Human 1mmune/haema	Human secreted pro	Human secreted pro	Human nervous syst	Propionibacterium	Homo sapiens sprou	Maize resistance g	Human ORFX ORF948	Homo sapiens sprou	Human SPROUTY prot	Human SPROUTY-1 pr	Sorghum resistance	Polypeptide isolat	Human SPROUTY prot	Human SPROUTY-1 pr	Human SPROUTY-1 pr	Human SPROUTY-1 pr	Human polypeptide	Amino acid sequenc	Human polypeptide	Human SPROUTY-1 pr		Arabidopsis thalla
ABG09140	AAR84882	AAW40057	AAR79054	AAW40058	AAY94252	ABB44555	ABB44556	AAB84634	ABB70437	AAM86342	AAW74947	AAW74790	ABB15777	AAU56930	AAW48794	AAY 58843	AAB41184	AAW48793	AAY87596	AAY87595	AAY58851	AAB19104	AAY87597	AAY87592	AAY87593	AAY87591	AAM38688	AAB64377	AAM4 04 74	AAY87594	AAG23211	AAG23210
22	16	19	16	19	21	22	22	22	22	22	19	19	22	22	19	21	21	19	21	21	21	21	21	21	21	21	22	22	22	21	21	71
316	2414	2414	2441	2441	2441	2441	2442	3190	3275	57	9	61	90	100	117	136	139	140	156	167	172	174	288	294	295	319	319	319	326	338	423	485
71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	4.69	69.4	69.4	69.4	69.4	69.4
35	32	35	35	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
12	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fundicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; anglogenesis; cerebrovascular disorder; nevous system disorder; anglogenesis; wound healing; skin aging; food additive; preservative.
                                                                                                                    Human secreted protein sequence encoded by gene 34 SEQ ID NO:94.
                            AAB44795 standard; Protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999; 99US-0126597.
07-JAN-2000; 2000US-0174877.
                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000WO-US07726.
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                   WO200058336-A1.
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                     12-FEB-2001
                                                                                                                                                                                                                                                                                                                               05-OCT-2000.
                                                         AAB44795;
RESULT 1
               AAB44795
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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                                                                                                          The polynuclectide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. AAB44812 to AAB44892 represent human secreted polypeptide sequences and proteins conditions to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities are:

Condition Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities are:

Conforted to an interthritic; antibacterial; variathmentic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;

Conforted to ameliorate a medical condition in e.g. humans, mice, prevent, treat or ameliorate a medical condition in e.g. humans, mice, cabbits, poats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmum diaseases, hyperproliferative disorders, cardiovascular disorders, and ocular disorders, cardiovascular disorders, and ocular disorders, and so used to aid wound healing and ceptihelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of polypeptides can also be used to aid wound healing and ceptimary tissues to regenerate tissues and in chemotrais. The condition of the present incention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antishumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; andiogenesis; cerebrovascular disorder; nervous system disorder; andiogenesis; wound healing; skin aging; food additive; preservative.
                           Nucleic acid encoding human secreted proteins, used to treat, prevent, ameliorate or diagnose medical conditions such as cancer, and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 34 human secreted protein homologous amino acid sequence #119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 74; 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 2
Pred. No. 38;
1; Mismatches
                                                                                     Claim 11; Page 368-369; 391pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB44820 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.68;
75.08;
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07-JAN-2000; 2000US-0174877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AA;
N-PSDB; AAC79832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 EKYCCSPK 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB4462 to AAB44811. AAB44812 to AAB44829 represent human secreted polypeptide sequences and proteins compared to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities are: immunosuppressive; antiarthritic; antirheumatic; antiprolliferative; cytostatic; cardiant; vasotropic; errebroprotective; nootropic; cytostatic; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperprollferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system clisorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; anglogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC79790 to AAC79798 and AAB4761 represent sequences used in the exemplification of the present
                                                                                                                                                    Nucleic acid encoding human secreted proteins, used to treat, prevent, ameliorate or diagnose medical conditions such as cancer, and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein sequence encoded by gene 34 SEQ ID NO:120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 379-380; 391pp; English.
Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB44821 standard; Protein; 119 AA.
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75.0%;
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Best Local Similarity 75.0
احت مریاتی
                                                                              WPI; 2000-602355/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA;
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Rosen CA,
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Matches
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ABB69460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Invention, numan secreted processed in. Examples of activities are:

and cells the genes are expressed in. Examples of activities are:

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;

Cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;

neuroprotective; antibacterial; virucide; fungicide; and

pervent, treat or ameliorate a medical condition in e.g. humans, mice,

rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used

in diagnosing a pathological condition or susceptibility to a

pathological condition. Disorders which are diagnosed or treated include

autoimnume diseases, hyperproliferative disorders, cardiovascular

disorders, cerebrovascular disorders, angiogenesis, nervous system

disorders, infections caused by bacteria, viruses and fungi and ocular

disorders. Infections caused by bacteria, viruses and fungi and ocular

disorders. The polypeptides can also be used to aid wound healing and

epithelial cell proliferation, to prevent skin aging due to subburn, to

maintain organs before transplantation, for supporting cell culture of

polypeptides can also be used as a foremeaxis. The

conjections caused as a discussion of the present

conference or decrease storage capabilities. AAC79798 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                               The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. AAB44812 to AAB44829 represent human secreted polypeptide sequences and proteins homologous to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                      Nucleic acid encoding human secreted proteins, used to treat, prevent, ameliorate or diagnose medical conditions such as cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 39; DB 21; Length 119; 75.0%; Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                           Oisclosure; Page 380; 391pp; English.
                                                                                                      Ruben SM, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG74903 standard; Protein; 124 AA.
                                                                            (HUMA-) HUMAN GENOME SCI INC
          23-MAR-2000; 2000WO-US07726.
                                   26-MAR-1999; 99US-0126597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal carcinoma
                                                                                                                                                                     ameliorate or diagno
autoimmune diseases
                                                                                                                             MPI; 2000-602355/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 EKYCCSPK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OKYCCSRK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200122920-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG74903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens have cytostatic activity and can be used in gene therapy and vacchae production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell on express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 39; DB 22; Length 124; 75.0%; Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 7210-7211; 9803pp; English.
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                                                                                                                                                                                                                                    Birse CE,
                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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11-JUL-2000; 2000US-0614150.
28-SEP-2000; 2000WO-US26524.
                                                               99US-0157137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                    Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                               WPI; 2001-235357/24.
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                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH34308
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                                                               29-SEP-1999;
03-NOV-1999;
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73.5%;
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2000US-0649167.
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                                                                                                                                                                                                                                                            (first entry)
                                                                                                              Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73
                                                                                109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS91280
                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                        22 KYCCSK 27
                                                                                                                                            2 KYCCSR 7
                                                                                                                                                                                                                                                          18-FEB-2002
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity
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                                                                                 Sequence
                                                                                                   Query Match
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                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell:cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents E. maxima T-lymphocyte stimulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding Eimeria T-lymphocyte stimulatory protein - used in sines to protect poultry against coccidiosis, and to develop is. for diagnosis of Eimeria infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. maxima; T-lymphocyte stimulatory protein; Eimeria; protozoan;
coccidiosis; chicken; vaccine; poultry; probe.
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O
                                                                                                            Disclosure; SEQ ID NO 35172; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                              22; Length 58;
                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           DB (
                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                             Score 36;
Pred. No. 9
                    Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomley FM,
                                                                                                                                                                                                                                                                                                                                                                                           AAR84086 standard; Protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-lymphocyte stimulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 46; 59pp; English
                    Li PWD,
                                                                                                                                                                                                                                                                              73.5%;
71.4%;
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                                                                                                                                                                                                                                                                                                  5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALKU ) AKZO NOBEL NV.
                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-210114/22.
                                       WPI; 2001-656860/75
(PEKE ) PE CORP NY
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Best Local Similarity
Matches 5; Conserv
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                                                  N-PSDB; ABL13563
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                                                                                           interactions
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C Elimeria protecomes are the cause of concellionals in chickens, the DMA emochain this sequence may be attached to a suitable promoter and used concellional this sequence may be attached to a suitable promoter and used concellional transcriptors. Frequents of this sequence may also concellionals. Frequents of this sequence may also concerned and used of positive quality spaints concellionals. Frequents of this sequence may also concerned and used on the corresponding DMA sequence. Sequence is a sequence as a sequence is a sequence in the corresponding DMA sequence. Binary and the corresponding DMA sequence. Binary as a sequence is a sequence in the corresponding DMA sequence. Binary as a sequence is a sequence in the corresponding DMA sequence. Binary and sequence is a sequence in the corresponding DMA sequence. Binary and sequence is a sequence in the corresponding DMA sequence. Binary and sequence is a sequence in the corresponding DMA sequence is a sequence in the corresponding DMA sequence. Binary and sequence is a sequence in the corresponding DMA sequence is a sequence in the corresponding DMA sequence. Binary and sequence is a sequence in the sequence is a sequence in the corresponding of the sequence is a sequence in sequence in sequence in sequence is a sequence in sequence in the sequence is a sequence in sequence in sequence in sequence is a sequence in sequence in sequence in sequence is a sequence in sequence in sequence in sequence is a sequence in sequence in sequence in sequence in sequence is a sequence in sequence in sequence in sequence is sequence in sequence is sequence in sequence is sequenced in seq
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Query Match

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Matches

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AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                     Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum; tobacco plant; osmotin gene; promoter; inhibition; fungal pathogen; insect pathogen; nematode pathogen; viral pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 35; DB 20; Length 189; 100.0%; Pred. No. 3.2e+02; vative 0; Mismatches 0; Indels
                                                                                                                                  Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 714-715; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                 AAY34717 standard; Protein; 189 AA.
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97FR-0014673
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                                                                                                                                                                                                                                              Chlamydia pneumoniae.
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21-NOV-1997;
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                                                                                              13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffais R;
                                                           AAY34717;
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AAW69751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human myelin P0 protein 14 (I). (I) has cytostatic, immunomodulatory, haemostatic, anti-HIV and antiinflammatory estivities. (I) and the polynucleotide encoding it are applicable in the diagnosis and treatment of malignant neoplasm, haemopathy, HIV infection, immunological diseases and various inflammations.
amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; myelin PO protein 14; cytostatic; immunomodulatory; haemostatic; anti-HIV; antiinflammatory; diagnosis; malignant neoplasm; haemopathy; HIV infection; immunological disease; inflammation.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myelin PO protein 14 and encoded polynucleotide, applicable in diagnosis and treatment of malignant neoplasm, hemopathy, HIV infection, immunological diseases and various inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                        0;
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                                                                                                                                                  Length 505;
                                                                                                                               73.5%; Score 36; DB 22; Length 50
71.4%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 22; L. 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYFU-) UNIV FUDAN.
(SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human myelin P0 protein 14 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                        AAB99956 standard; Protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 29; 37pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-2000; 2000WO-CN00668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                      5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                322 KYCCSQQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH44460
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QKYCC 112
                                                                                                                                                                                                                         2 KYCCSRK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001
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                                                                                                               Sequence
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Gaps ;;

108

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RESULT 9

us-09-606-129a-35.rag

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31-MAR-2000;
23-AUG-2000;
                                               12-JAN-1994;
                                                                         12-JAN-1994;
20-MAY-1993;
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  US5874626-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method has been developed of inhibiting a pathogen in a plant. The method comprises: (a) providing or constructing a vector comprising an osmotin promoter and foreign DNA sequence encoding a pathogen-inhibiting protein, where the promoter is operably linked to the foreign DNA sequence and includes: (i) nuclectide sequence 5 of the osmotin coding sequence and includes: (i) nuclectide sequence 6 for the osmotin coding sequence, the coding sequence faithed as tarting at bp 2034 of the 3033 bp osmotin sequence (see AAV52754), (ii) a nuclectide sequence which hybridises to (i) and promotes expression of an operably introducing the vector into the plant to create a transformed plant, where expression of the pathogen-inhibiting protein in the transformed plant is regulated by the osmotin promoter. The method is useful for the plant is regulated by the osmotin promoter. The method is useful for the production of recombinant plants having genes under control of an osmotin promoter, especially of pathogen inhibiting proteins. Osmotins are cationic plant proteins, similar to tobacco PR-5-type proteins. The osmotin genes are under control of hormonal or environmental signals, including abscisic acid, ethylene, tobacco mosalc virus invention, callintly, desiccation and wounding. The present sequence represents the Nicotiana tabacum osmotin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                            Inhibition of pathogens in plants by recombinant expression of pathogen inhibiting proteins - uses nucleic acid constructs containing the pathogen inhibiting proteins under control of osmotin promoter, which is inducible by specific signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
            /note= "encoded by GGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                        Claim 1; Column 29-34; 26pp; English.
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                                                                                                          94US-0180428.
93US-0065147.
95US-0482037.
                                                                                   95US-0482037
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                                                                                                                                                           (PURD ) PURDUE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                   Bressan R, Hasegawa PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco osmotin protein.
                                                                                                                                                                                                        WPI; 1998-494773/42.
Misc-difference 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum.
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                                                                                                                                                                                                                      N-PSDB; AAV52754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OKYCCSRK 8
                                                                                                          12-JAN-1994;
20-MAY-1993;
07-JUN-1995;
                                                                                   07-JUN-1995;
                                   US5801028-A
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                                                           01-SEP-1998
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The present sequence represents the Nicotiana tabacum (tobacco) osmotin protein. The present invention specifically claims a DNA fragment comprising the osmotin gene promoter sequence with no more than 100 bp of the coding sequence. Also described are methods which are useful in processes for achieving expression of a coding sequence from a foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                           Tobacco osmotin gene promoter – and recombinant construct comprising foreign gene under its control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG09140 standard; Protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9A; 26pp; English.
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2000US-0649167.
94US-0180428
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                                                                               93US-0065147
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                                                                                                                                          (PURD ) PURDUE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                   Bressan R, Hasegawa PM;
                                                                                                                                                                                                                                                        WPI; 1999-180080/15.
N-PSDB; AAX16340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene in a host cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 QOYCCTOR 181
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95WO-US04682
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                                                                                                                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; diagnosis.
                                                                                                                                                                                                                                                                   345 AA;
                                                                                                                                                                                                                                                                                                                                                                 306 YCCSRE 311
                                                                                                                                                                                                                                                                                                                                                 3 YCCSRK 8
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                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR84882;
                                                                                                                                                                                                                                                                                              Query Match
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AAR84882
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                                                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical magning of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                and to produce other types of data and products dependent on DNA and mainto acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signaling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eucalyptus grandis cell signalling involved protein SEQ ID NO:802.
                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 22; Length 316;
Pred. No. 4.8e+02;
1; Mismatches 0; Indels
                                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                        Claim 20; SEQ ID No 39499; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB25483 standard; Protein; 345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                        71.48;
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99US-0162866
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                               316 AA;
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276 FCCSRK 281
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 blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiate also known as Monteey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external cevelopment of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance altered fruit rad be used to delay senescence in selected cell types or cogans providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
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/label- C/H-rich_region_1
/label- C/H-rich_region_1
/note= "cysteine/histidine-rich region containing
2 putative zinc finger motifs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%; Score 35; DB 21; Length 345; 83.3%; Pred. No. 5.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Nuclear_location_signal
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/label- C/H-rich_region_2
1622..1821
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Claim 3; Page 371-372; 527pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR84882 standard; Protein; 2414 AA.
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                       Nucleic acid encoding human p300 that associates with adenovirus ElA. - and related vectors, host cells and screening assays, also diagnosis of cancerous and pre:cancerous tissue by detection of
                                                                                                               Transcription factor p300 was isolated from human 293 cells and used to generate polyclonal antisera in mice. These were used to screen 293 cDNA libraries to isolate clones contg. overlapping inserts, which were assembled to obtain a full-length cDNA sequence (AAT02792) encoding a protein (AAR84882) of predicted mol.wt. 264.236 kDa. p300 may be produced in host cells (pref. mammalian) and used to modulate p300-dependent transcription.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide sequence comprises p300, a global transcriptional coactivator that is involved in the regulation of various DNA-binding transcriptional factors. The invention relates to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular transcriptional factor; p300; human; P300; P/CAF; transcription; histone acetyltransferase; HIV; infection; cancer; therapy; muscle differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated p300/CBP-associated factor, P/CAF - used to develop products for modulating transcription, e.g. for treating HIV infection or cancers or for promoting muscle differentiation
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Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 76-81; 107pp; English.
                                                                                         Disclosure; Page 61-78; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular transcriptional factor p300.
                                                                                                                                                                                                                                                                                                                                                                                                        AAW40057 standard; Protein; 2414 AA.
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1763..1966
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1998 (first entry)
                                                                                                                                                                                                                                                             Query Match 71.4
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                     2414 AA;
N-PSDB; AAT02792
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CC modulates transcription through binding to p300 and CDPC (See AMW40058). The region (see AWW40055) of p300 that binds to P/CAF (See AWW40058). The region (see AWW40055) of p300 that binds to P/CAF (See AWW40058). The region (see AWW40055) of p300 that binds to P/CAF (See AWW40058). The region (see AWW40055) of p300 that binds to P/CAF (See AWW40058). The invention provides methods of screening for compounds that inhbit or stimulate the transcription modulating CC and histone acetyltransferase activity of P/CAF and p300/CBP. CC Inhibitors can be used e.g. to inhibit HIV TAT-mediated concer or to activate tumour suppressor p53 in the treatment of CC cancer or to activate the muscle differentiation. The products can also be used to promote muscle differentiation. The products can also be used to concerting the sample brinds p300/CBP in a subject. Also provided is concerting the sample with the P/CAF binding region of p300 and CC determining the amount of P/CAF in a sample by CC determining the amount of P/CAF in a sample by CC determining the amount of P/CAF binding region of p300 and XX Sequence 2414 AA;

Outery Match

Outery Match

De 1162 YCGSRK 8

Search completed: November 1, 2002, 14:47:10

Search completed: November 1, 2002, 14:47:10
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(without alignments)
952.238 Million cell updates/sec
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1508
1 MNAEPERKFGVVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

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sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_invertebrate:* sp_virus:*
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sp_unclassified:* sp_organelle:* sp_phage:* sp_plant:* sp_rvirus:*
sp_bacteriap:* sp_archeap: * sp_rodent:* sp_mammal:* sp_mhc:* SPTREMBL_19:* 10: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
SO.	Score	Match	Match Length DB ID	DB	CI	Description
7	1494	99.1		4	Q96QL4	Q96q14 homo sapien
7	1484	98.4		4	Q9BRW8	Q9brw8 homo sapien
Э	1253.5	83.1		11	Q9CY64	Q9cy64 mus musculu
4	1253.5	83.1		11	Q9DD21	O9dd21 mus musculu
Ŋ	450	29.8		4	095019	095019 homo sapien
9	218.5	14,5		16	P72782	P72782 synechocyst
7	155.5	10.3		17	0970н0	097uh0 sulfolobus
80	142.5	9.4		16	Q986T3	Q986t3 rhizobium l
თ	142	9.4	318	17	026961	026961 methanother
10	139	9.5		16	P94437	P94437 bacillus su
11	133	8.8		16	Q9WZ54	Q9wz54 thermotoga
12	132.5	8.8		10	023580	023580 arabidopsis
13	131.5	8.7		16	Q9CFC7	09cfc7 lactococcus
14	130.5	8.7		16	Q98DB4	Q98db4 rhizobium l
15	129	8.6		2	Q9VQB3	Q9vqb3 drosophila
16	128.5	8.5	368	က	042896	042896 schizosacch

181 GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240 

LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLF 180

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117 11 18 18 18 18 18 18 18 18 18 18 18 18	013991 093764 092705 092705 092773 099X04 099X04 099X04 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 091CW9 09	ALIGNMENTS PRT; 296 A Created) Last sequence Last sequence 06). Craniata; Ve Craniata; Ve Craniata; Ve Craniata; Catarrhini; Catarrhini; Last AmburgenBank/D
117 11 18 18 18 18 18 18 18 18 18 18 18 18		19, 119, 119, 119, 119, 118, 118, 118, 1
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MEDLINE-21085660; PUDMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SHEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLLYSLF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1
              241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 296;
                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Jisson R., Strausberg R., Strausberg R., Strausberg R., Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005902; ARH05902.1; -. InterPro; IPR006883; GFO_IDH_MocA. InterPro; IPR0408; GFO_IDH_MocA, Issource 296 AA; 33432 MW; A389AFDDB6ADBABF CRC64;
                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%; Score 1484; DB 4;
98.3%; Pred. No. 3.9e-115;
ive 2; Mismatches 3;
                                                                                                                                                           296 AA
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=BRAIN, PRIMITIVE NEUROECTODERMAL;
                                                                                                                                                                                                    Created)
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                                                                                                                                                           PRT;
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01-JUN-2001 (TrEMBLEE). 17,
01-JUN-2001 (TrEMBLEE). 17,
2500001N03RIK PROTEIN.
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                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Matches 291;
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                                                                                                                                                         Q9BRW8
                                                                                                                                                                                Q9BRW8
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                                                                                                                RESULT 2
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Radto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Releischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L., Staubli F., Sızuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,
Roustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.1%; Score 1253.5; DB 11; Length 295; 82.9%; Pred. No. 5.1e-96; ive 28; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 VPNVGVNKNIFLKDQDIFIQKLLGQVSAEDLAAEKKRILHCLELASDIQRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F2E1682BD77032A4 CRC64;
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Last annotation update)
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MEDLINE=21085660; PubMed=11217851;
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MGD; MGI:1917355; 2500001N03Rik.
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SEQUENCE 295 AA; 33524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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0610006A11RIK.
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KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVS 178
                                                                                                 179 LFGELSLVSATLEERKEDOYMKMTVCLETEKK
                                                                                                                    LFGELSLVSATLEERKEDQYMKMTVCLETEKK
                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                05,
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                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       BILIVERDIN REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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SEQUENCE 328 AA;
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                          119
                                                                                                                                                                                         RESULT 6
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujite M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S., "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GELSLISATMENRKEDQYMKMIVQLETQNKSPLSWIEEKGPGLKRNRHISIHFKSGSLEE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVOQISLE 60
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         DB 11; Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 VPNVGVNKNIFLKDQDIFIQKLLGQVSAEDLAAEKKRILHCLELASDIQRLC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYC
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                                                                                                                                                                                                                                                                                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cordes M., Wohldman P., Morris M.;
"The sequence of Homo sapiens PAC clone RP5-974M14.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                     Nature 409:685-690(2001).

EMBL; AK002231; BAB21950_1; ...

MGD; MGI:1915580; 06100066A11Rik.

InterPro: IPRO00689; GFO_IDH_MOCA.

Fram; PF0408; GFO_IDH_MOCA; 1.

SEQUENCE 303 AA; 34491 MW; 52D8A3B02EE956EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 92
92 AA; 10552 MW; 390331108449BD93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BILIVERDIN-IX ALPHA REDUCTASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 450; DB 4;
Pred. No. 4.5e-30;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                       83.1%; Score 1253.5; DB 82.9%; Pred. No. 5.3e-96;
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                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
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01-WAY-1999 (TrEMBLrel. 10, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC004939; AAD05025.1;
                                                                                                                                                                                                                                                                                                                                                                         Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 96.7
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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SEQUENCE
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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095019
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGISRLTWLVSLFGELSLVSATLE--ERKEDQYMK---MTVCLETEKKSPLSWIEEKGPG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 KGKVLHEEHVELLMEEFAFLKKEV--VGKDL-LKGSLLFTSDPLEE-----DRFGFPAF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSID-----GVQ-Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).

EMBL: D90900; BA16797.1; -.

InterPro: IPR0010683; GFO_IDH_MocA.

InterPro: IPR001044; GFO_IDH_MocA.C.

Pfam; PF01408; GFO_IDH_MocA.C. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium
8 ATPVR----VGIVGTGYAAQRRAEVFRGDRRS----QLVSFWGNSEANTAKFADTFGVRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 LKRN-RYLSFHFKSGSL------ENVPNVGVNKNIFLKDQNIFVQKLLGQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AALSRISRFTDLFGTVQQVDAQCRFWDQPNPEYFRACLATAYLQFNNGLKAEVIYGKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 218.5; DB 16; Length 328; 25.2%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 AA; 36640 MW; 51474ABD26B2C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                    RECORDENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

X MEDLINE=21332296; PubMed=11427726;

X MEDLINE=21332296; PubMed=11427726;

X She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Menkamp-de Jong I., Jeffrias A.C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffrias A.C., Kozera C.J., Medina N., Peng X.,

Thi Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RL EMBL; AE006895; AAK41149.1;

DR EMBL; AE006895; AAK41149.1;

DR InterPro; IPR000683; GRO_IDH_MOCA_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GKVLHEEHVELLMEEFAFLKKEVVGKDL------LKGSLLFTSDPL---- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWIEEKGPGLKRNRYLSFHFKSGSLENVPNV-------GVNKNIFLKDQNI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 --VEDTAVAIMR-----YKNGALGTISQTVSMKPTTYQYRKIRVNGSNGFVEITDGSL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 RKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSR-----RELGSIDGV-QQISLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 KRIGVAVVGLGSIGKTHVKALKDLEKETEFVKLVAVVDQIKAIAEKIGSEYGTPYYTTID 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 RGMWNTEGGGVMTNQGIHTIDLMIWLNGEVEEVSGFVDNLTHDG-----IE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16,
                                                                                                                  Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         371 AA; 41760 MW; DAAE16466D53306B CRC64;
                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 155.5; DB 1720.6%; Pred. No. 8.3e-05;
371 AA
                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pfam; PF02894; GFO_IDH_MOCA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 FVQKLLGQFSEKELAAEKKR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |: | |:
288 STVAIEGKIEESKSSVEYKK 307
                         01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
PRELIMINARY;
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                                                                     DEHYDROGENASE, PUTATIVE.
                                                                                                  Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                NCBI_TaxID-2287;
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Local Sim.
66;
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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:| : :: || |:: : :: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 ---GVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 DRF---GFPAFS-GISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSW 215
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Methanothermobacter.
NCBI_TaxID=145262;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-CHLOROBENZOATE-3,4-DIOXYGENASE DYHYDROGENASE RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Mismatches 104; Indels
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EMBL; ARB000863; AABB8373.1; ...
InterPro; IPR00683; GFO_IDH_MocA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 382 AA; 40593 MW; 785DA27E3D3308C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4%; Score 142.5; DB
4.1%; Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:331.338(2000).
EMBL; AP003011; BAB53370.1; -.
InterPro; IPR000683; GFO_IDH_MocA.
Pfam; PF01408; GFO_IDH_MocA: 1.
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MEDLINE=98037514; PubMed=9371463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 24.18;
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23,3%;
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 23.3
Matches 65; Conservative
                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 393 AA;
                                                                                                                                                                                                                STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9WZ54
Q9WZ54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TM0585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto H., Uchiyama S., Sekiguchi J., ^{\circ} ^{\circ} ^{\circ} The Bacillus subtilis chromosome region near 78 degrees contains the genes encoding a new two-component system, three ABC transporters and
                                                                                                                                                                                     ||| : : :|:| |: |
121 GHVERFNPAVQKAKELIENDVIG-DVVSASAKRVGPFPPRIKDVGVTIDLAIHDLDVMHY 179
                                                                                                                                                                                                                                                                               151 LFTSDPLEE-----VSLFGE 182
                                                                                                                                                                        SSOEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEOKGKVLHE 123
                                                                                                                                                                                                                                                                                                         LF-SEPVAEVYAVMGSILEKCEYEDHAEIMTKFK-SGITGILEVNWLTPYKRRKLAITGT 237
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Burschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guisepi G., Guy B.J., Haga K., Halbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Klein C.,
                                                                                                                     7 RKFGVVVVGVGRAGSVRMR---DLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDAL 63
                                                                                                                                             2 RQINVCVIGVGAMGYNHARVYYRLKNAN-LMAVSDIMKGTLQKVANKYDTVGYVDYENLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Madigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                          68;
                                                                9.4%; Score 142; DB 17; Length 318; 21.0%; Pred. No. 0.00088; ive 50; Mismatches 96; Indels 66
                                                                                                                                                                                                                            124 EHVE----LLMEEFAFLKKEVVGKDLLKGS--------
Pfam; PF01408; GFO_IDH_MocA; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
Dioxygenase; Complete proteome:
SEQUENCE 318 AA; 35653 MW; 3145C2169A98D1E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                              393 AA
                                                                                                                                                                                                                                                                                                                                   183 LSLVSATLEERKEDQYMKMTVCLETEKKSPL 213
                                                                                                                                                                                                                                                                                                                                                  238 DGIINVDYIDQRLDVYGKFAQDVDIKHEEPL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus group; Bacillus.NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 03, (TrEMBLrel. 03, (TrEMBLrel. 19,
                                                                              1 Similarity 21.0° 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE FROM N.A.
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01-DEC-2001
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                                                                  Query Match
                                                                               Best Local
Matches 5
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Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Saconlan E., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Soriokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin, A.; Subtils.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 QTMFAEEAKRQDGIEVVSIATPNGTHYEICKAALEAGVHVICEKPLFFTSAEGQEIKALA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQKGKVLHEEH----VELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGF----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 EKISAAQKWRVDPAIAGPS-----FVLGDLS-----THTYYMSOLIMPKMKIKEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 QQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELA 114
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STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
MELSON K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VVGVGRAGSV----RMRDLRNPHPSSAF-LNLIGFVSRRELGSIDGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 139; DB 16; Length 393; 33.3%; Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; D78508; BAA11399.1; -.
EMBL; Z99108; CAB12657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 AA; 43584 MW; 3EEE326E1A047602 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN BPLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 L----SWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 LCDRQSFVGSRAP-LEDNAHVLMHYENGAVGTMWTSSIN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000683; GFO_IDH_MocA.
InterPro: IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
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NCBI_TaxID=2336;
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9

13;

Length 364;

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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                      52 DGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGK--HVLVEYPMTLSLAAAQE 109
                                                                                                                                                                                                                                                                                                                                                                                                                          67 SG-----HEELLKSELCDVIVVSSPNMTHHQILMDIINYSKPHHVLVEKPLCTTVADCKQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PVCVMASGGMDVNHK 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFGVV------VVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQIS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                    110 LWELAEQKGKVLHEEHVEL-LMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KFGVVVVG-VGRAGSVRMRDLR------NPHPSSAFLNL-----IGFVSRRELGSI
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Pred. No. 0.0067;
....rrhas 88; Indels
                                                                                                                                                                                                                                                                             Indels
                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 297343; CAB10518.1;
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR04104; GFO_IDH_MocA.
InterPro; IPR044104; GFO_IDH_MocA.C.
Pfam; PF01408; GFO_IDH_MocA.C.
SEQUENCE 364 AA; 40260 WW; B56312BD6CF01B95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       Score 132.5; DB 10;
Pred. No. 0.0066;
50; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF01408; GFO_IDH_MocA; 1.
Complete protecome.
SEQUENCE 324 AA; 36603 MW; DBF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GLNKMGLWTLVEKCCHFFDLMRLFAGAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 EE----KGPGLKRNRYLSFHFKSG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | : | : | : | : | 221 DEVYGGKVPDIIDNAYVIIEFDNG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
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                                                                                                                                                                                                                                        8.88;
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                                                                                                                                                                                                                                                          22.7%;
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                                                                                                                                                                                                                                                          Local Similarity 22.7% tose 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Nature 391:485-488(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                    SEQUENCE FROM N.A.
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01-OCT-2001
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Q9CFC7
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MEDLINE-9812113; PubMed=9461215;
MEDLINE-9812113; PubMed=9461215;
MEDLINE-9812113; PubMed=9461215;
MEDLINE-98121113; PubMed=9461215;
MEDLINE-98121113; PubMed=N. Love K., Goodman H., Dean C.,
METAL Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
Medler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
A. Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
A. Silvey M., James R., Montfort A., Pons A., Piravandi E., Obermaier B.,
A. Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
A. Belseny M., Volckaert G., Mewes H.W., Klosterman S.,
Schueller C., Chalwatzis N.;
A. Arabidopsis thaliana.";
                 Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             S9 TWINYRELLKREDVDVISIATESGKHYQITWEALEAGKHVLVEKPMALSTKHMNEWVELS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                            --ISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LKLGVFF-----QNRFNPPVQEVRKKLD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 --SGAFGKIFYASVAVRWNRNEDYYKQA-----SWRGTWEMDGGVLMNO--STH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLT 174
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                   8 KFGVVVVGVGRAGS-----VRMRDLRNPHPSSAFLNLIGFVSRRELGSID--GVQQ-- 56
                                                                                                                                                                                                                                                                                                                                                                                      2 KLRIALVGCGRIGQKKHVPALIETQDL---FETVAVCDLVEERANRAAEHFEKSGLRRPE 58
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 WLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSW--IEEKGPGLKRNRYLSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INOSITOL 2-DEHYDROGENASE HOMOLOG (INOSITOL 2-DEHYDROGENASE LIKE
                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                           Length 360;
                                                                                                                                                                                                                                       360 AA; 41023 MW; 3B17BCD4A94A6EC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AIDLLQWFLGGEIEEIYGHIANTNHPYIEAEDEGFAIVKFKG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 -----FKSGSLENVPNVGVNKN---IFLKDQNIFVQKLLG 264
                                                                                                                                                                                                                                                                                              ; Pred. No. 0.0059; 38; Mismatches 103;
                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                            8.8%; Score 133; DB 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 AA
                                                                                                                      InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
InterPro; IPR003409; Ribosomal_S30.
Pfam; PF01408; GFO_IDH_MOCA; 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05, Created)
05, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                     EMBL; AE001733; AAD35670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                              23.0%;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                        Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                       Complete proteome. SEQUENCE 360 AA;
                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 KOKN-----
                                                                                                            TIGR; TM0585;
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223580;
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CG3597 PROTEIN
                   CG3597
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                   ---DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAA 107
                                         DLLKGS---LLFTSDPLEEDRF----GFPAFSGISRLTWLVSLFGELSLVSATLEERKED 196
                                                                                                                                                                                                              19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQ----QIS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                         -----QYMKMTVCLETEKKSPLSWI--EEKG----PGLKRNRYLSFHFKSGSLE 239
                                                                                                                                                                                                                                                                                               208 LDYEILLKKAEIMINISLSTRLDKPNTFIIYGEKGEISVPNYWKSNQASLIKNDGTVE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 130.5; DB 16; Lengtm
30.5%; Pred. No. 0.0091;
... wiematches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 AA; 38205 MW; D134AEAB87F547ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                  QELWELAEQKGKVLHEEHVELLMEEFAFLKK----EVVGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                         351
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InterPro; IPR000683; GFO_IDH_MocA.
Pfan; FF01408; GFO_IDH_MocA; 1.
Complete proteome. 38105 MW; D134
SEQUENCE 351 AA; 38205 MW; D134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 KKLVIGYILRHHPSWIRLIAE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KVL-----HEEHVELLME 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 30.5%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLR4777 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-381;
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       Q98DB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09VQB3
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Q9VQB3
                                                                                                  108
                                                                                                                                                                                                                             164
                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
Q98DB4
                 29
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Radams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Radadon R.C., Rogers Y.-H.C., Blazej R.G., Chango O., Chen L.X.,
RA Adamon J.R., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pennokoh C., Baldwin D.,
Radion R.C., Busch R., Bavendale J., Bayrsktroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chadra I.,
RA G. Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dittler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chadra I.,
RA Cawley S., Dahlke C., Davisenor E., Dunkov B.C.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chadra I.,
RA Cablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dittler P.,
RA Burtis K.C., Gargin R.S., Galbart W.M., Glasser K.,
RA Burtis K.C., Gargin R.S., Galbart W.M., Glasser K.,
RA Gerleck A., Gorg N.S., Galbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heinman Y.S., Galbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heinman T.J., Weil M.-H., Ibegwam C.,
Liu X., Mattei B., McIntoh T.J., Weil M.-H., Ibegwam C.,
RA Melson D.R., Moy M., Murphy B., Murphy L., Murshy D.M., Nepherson D.,
RA Melson D.R., Naten G.S., Pan S., Pollard J., Wolferson D.,
Radior C., Siden-Klamos I., Simpson M., Strong R., Parcel B.,
Radior C., Siden-Klamos I., Simpson M., Strong R., Wang X.,
Waller E., Spadling A.C., Stapleton M., Strong R., Wang X.,
Waller E., Spadling A.C., Stapleton M., Strong R., Sun E.,
Radior R., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
Waller R.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Radior R.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Radior R.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Radior R.M., Woodage T., Worley K.C., Wu D., Yang S.
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Drosophila melanogaster (Fruit fly).
Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidee; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 129; DB 5; Length 335; 77%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam: PF01408; GFO_IDH_MOCA.1.
SEQUENCE 335 AA; 37812 MW; EIAEB59E5F270612 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||: ||||: | | | | : | : | | ELYTLAEQRGVFIMEGMWSRFFPSYDRLRELLKNDVIGE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
                                                                                                                                                                                                                                                                                           STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0031417; CG3597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.78;
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Best Local Similarity
                                                                                                                                                                                                                                                 SEOUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=7227;
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; 9

Search completed: November 1, 2002, 14:49:42 Job time: 56.7749 secs

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November 1, 2002, 14:41:32; Search time 15.2283 Seconds (without alignments) 752.611 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-606-129A-1 1508 1 MNAEPERKEGVVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P53004 home sapien P4684 rattus norv P4685 scherichia P74041 synechocyst 03222 bacillus su 005389 bacillus su 005389 bacillus su 005389 bacillus su P75931 escherichia 005184 pseudomonas 044258 comanonas t P4032 bacillus su P77376 escherichia 006189 accolaromy 007982 zymomonas m P47769 mycobacteri 006238 enterococcu P27059 astasia lon P54394 bacillus su 008378 home sapien P37168 salmonella P49305 rhizoblum m P02549 home sapien 062209 mus musculu P42599 escherichia P42599 escherichia P6259 escherichia P6259 escherichia P6259 scherichia
SUMMARIES	BIEA_HUMAN BIEA_RAT YHHX_ECOLI YHES_ECOLI YHES_ECOLI YHES_BACSU WINE_BACSU WINE_BACSU WINE_BACSU WINE_BACSU WINE_COLI PHT4_PSEPU CBAC_CONTE YISS_BACSU WM4_PSEPU CBAC_CONTE YISS_BACSU WM50_EVITO WM6_EVITO RM6_EVITO RM6_EVITO RM7_ECOLI YM6_EVITO WM10_EVITO WM10_EVIT
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SPCA_DROME UGA3_YEAST AKA9_HUMAN DEGS_BACBR BRE_STRAG MP1_TODAC RECG_AQUAE RECG_AQUAE SWCY_MOUSE YGB6_STRPN PURL_ACLA
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                               1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE 60
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
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                                                                                                                                                                                           BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                  100.0%; Score 1508; DB 1; 100.0%; Pred. No. 1.2e-108;
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SD -> AG (IN REF. 2
D -> E (IN REF. 2).
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MEDLINE-92156147; Pubmed=1371282;
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                                                                                                                        EMBL; AC005189; AAC25526.1; -.
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MCCOUDERY W.K. Jr., Maines M.D.;

Title-directed mutagenesis of cysteine residues in biliverdin
"Site-directed mutagenesis of cysteine residues in biliverdin
"Site-directed mutagenesis of cysteine residues in biliverdin
reductase. Roles in substrate and cofactor binding.";

Eur. J. Biochem. 222:597-603(1994).

-!- FUNCTION: CONVERTS BILIVERRIN TO BILIRUBIN: DISPLAYS TWO DISTINCT
PH OPTIMA USING A DIFFERENT COFACTOR AT EACH PH: NADH AT THE LOWER
PH 6.77-6.9 RANGE AND NADH AT PH 8:5-8.7. NADPH, HOWEVER, IS THE
PROBABLE COFACTOR IN BIOLOGICAL SYSTEMS.

-!- CATALYTIC ACTIVITY: BILILIRUBIN + NAD(P)(+) = biliverdin + NAD(P)H.

-!- PATHWAY: FINAL STEP IN HEME METABOLISM.

-!- PATHWAY: FINAL STEP IN HEME METABOLISM.

-!- SUBUNITY: MONOMER (BY SIMILARITY).

-!- SUBUNITY: TO E.COLI YHX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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219C8EA96C150588 CRC64;
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ZINC (POTENTIAL).
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C-AL LOSS OF ACTIVITY.
C->A: REDUCED ACTIVITY.
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                        le transcript product.";
Biol. Chem. 267:4023-4029(1992).
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Pfam; PF01408; GFO_IDH MocA; 1.
Oxidoreductase; NAD; NADP; Zinc.
PROPEP
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                                                                                                                           MEDLINE=94291657; PubMed=8020496;
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Synechocystis sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Gaps
                                                                                                                                    SEQUENCE FROM N.A.
STAIN-KIZ / MGISS;
MEDLINE=97426617: PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                           В.
                                                                                                                                                                                                                                                                           MEDLINE-99420866; PubMed-10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.
"Enrichment of low abundance proteins of Escherichia coli by
hydroxyaatite chromatography";
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 345;
                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Complete proteome.
SEQUENCE 345 AA; 38765 MW; 31D73A62511C7F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase sl10816 (EC 1.-.-.).
SLL0816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.1%; Score 152.5; DB 1; Best Local Similarity 31.3%; Pred. No. 0.00012; Matches 42; Conservative 27; Mismatches 52;
         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Putative oxidoreductase yhhX (EC 1....).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA
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:Dentification by MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EcoGene; EG12944; yhhx.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA, C.
Pfam; PF02894; GFO_IDH_MocA_C: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE000420; AAC76465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U18997; AAA58238.1; -.
                                                                                                                                                                                                                                       Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 LGVHTMDQIISLFG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGISRLTWLVSLFG 181
                                                                        Escherichia coli
                                                                                                              NCBI_TaxID=562;
                                                            YHHX OR B3440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y816_SYNY3
P74041;
                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
Y816_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).
-!- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
                                                                                                                                                                                                                                                                     Okumura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 GGGALGALASHTFDYLHWLFGPAQSLAANLSVAIAERPDPLDNNRLKPVTAEDTALISLT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- EVQVIPDFEFREVPAWQYVAELLGQGILGQLKLIKVDWLVGSRANPNRAWNWYAQREK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FGFPAFSGISRLTWLV----SLFGELSLVSATLEERKEDOYMK-------MT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQI-----SLEDA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 VAVIGTGFGQAVHIPALQYHQOTQAIA-----IYHRDLAKAQEVAKSNDLAYSYNNLEEL 63
                                                                                                                                                                   MEDLINE-97061201; PubMed-8905231; Kaneko I., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi I., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S. Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase in FHUD-OPUBD intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 134; DB 1; Length 371; 13.2%; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 23.2%; Pred. No. 0.0035;
Matches 64; Conservative 44; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA_C; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
Hypotherical protein; Oxidoreductase; Complete proteome. SEQUENCE 371 AA; 41489 MW; BDEFF020D4D848F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEHVELLME-EFAFLK-----KEVVGKDLLKGSLLFTSDPLEEDR-----
                                  Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 VCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
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(strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90911; BAA18116.1; -
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1423;
                                                                        NCBI_TaxID=1148;
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us-09-606-129a-1.rsp

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                              SWISS-PROT entry is copyright. It is produced through a collaboration
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MEDLINE=97177783; PubMed=9025289;
Gomez M., Cutting S.M.;
"Bofc encodes a putative forespore regulator of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAPAEIGGEDG---TIVIDT-----IHRPERVEIRYRDGREENIAIPDP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 VVLMEAMKTTFLPNFKELKKHLHKIGTVRRFTASYCQYSSRYDAFRSGTVLNAFQPELSN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FTSDPLEEDRFGFPAFSGISR----LTW----LVSLFGELSLV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114.5; DB 1; Length
Pred. No. 0.094;
46; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                  Subtilist; BG12388; yulf.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; PF01408; GFO_IDH_MocA, I.
Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 328 AA; 36515 MW; 53134AD13A4B2835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 NKNIFLKDQNIFVQKLLGQFSEKELAAEK---KRILHCLGLAEEIQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 143:157-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Clostridium group; sroup; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 KVLHEEHVELLMEEFAFLKKEV--VG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase yrbE (EC 1.-.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/
Bacillus/Staphylococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 252-341 FROM N.A.
                                                                                                                                                                                                                                         EMBL; Z93938; CAB07947.1; -. EMBL; Z99119; CAB15095.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.68;
Similarity 19.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.99
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oudega B., Koningsteyn G., Feger G., Pohl T.;
"Bacillus genome sequence project: sequence of mcp/tlp to yulf; a segment of the Bacillus genome at about 276 degrees.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY. STRONG, TO E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EITNDPAIELVIVTTPSGLHYEHTMACIQAGKHVVMEKPMTATAEEGETLKRAADEKGVL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTW---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGSI--VPANGPRYQIHGKDSSFIKYGIDGQ--EDALRAGR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKFGVVVVGV---GRAGSV---RMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKVDTIKVGILGYGLSGSVFHGPLLDVLDEYQISKIMTSRTEEVKRDFPDAEVVHE--LE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 IEEKGPGLKRNRYLSFHFKSGSLENVPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LVSLFGELSLVSATLEERKED----QYMKMTVCLETEKKSPLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 358;
                                                                                                                                                                                                                                                                                                                                                               Subtilist; BG14057; yvaA.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA_C.
Pfam; PF02494; GFO_IDH_MocA_C: 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 358 AA; 40112 MW; 532C4DB37CEB1570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 118.5; DB 1;
(0.9%; Pred. No. 0.052;
ve 52; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
14. MaRR-2002 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase yulf (EC 1. -. -.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 299121; CAB15358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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15-DEC-1998 (
15-DEC-1998 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YULF_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 K 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horluchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                    EVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVL---- 121
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                     13 VVGVGRAGSVRMRDL-RNPHPSSAFLNLIGFVSRRELGSIDGVQQI-----SLEDALSSQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattney F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                         126 RRFDPHFKKIKTIVE----NGEIGTPHLLK----ITSRDPEPPNIDYVRTSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coll.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                          7.4%; Score 111; DB 1; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 and the
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                               Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 341 AA; 37788 MW; E3023CD874F90C5F CRC64;
                                                                                                                                                                                                                                                                                                         79;
the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
homolog.
                                                                                                                                                                                                                                                                                         0.18;
                                                                                                                                                                                                                                                                                       22.2%; Pred. No. 0.18
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307
                                                                                                   STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                          Local Similarity 22.2
nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
Virulence factor mviM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLFGELSL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 -GLFMDMSI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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P75931;
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                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----HEEHVELLMEEFAFL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 KKEVV----GKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QISLEDALSS--QEVEVAYICSESSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWEL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LSWIEEKGPGLKRNRYLSFHFK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ITTCMHRRAGSQRETVQAVTDGALIDITDMREWREERGQGVVHKPIPGW--- 257
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 AARKKLTLMVGFNRRFAPLYGELKTQLATAASLRMDKHRSNSVGPHDLYFTLL-DDY1,HV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nomura Y., Nakagawa M., Ogawa N., Harashima S., Oshima Y.;
"Genes in PHT plasmid encoding the initial degradation pathway of
 the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 105.5; DB 1; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,5-DIHYDROXYPHTHALATE.
-!- PATHWAY: SECOND STEP OF PHTHALATE DEGRADATION.
-!- INDUCTION: INDUCED BY PHTHALATE AND REPRESSED BY GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phthalate in Pseudomonas putida.";
J. Ferment. Bioeng. 74:333-344(1992).
-!- FUNCTION: TRANSFORMS 4,5-DIHYDRO-4,5-DIHYDROXYPHTHALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Putative 4,5,-dihydroxyphthalate dehydrogenase (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                                             Virulence; Complete proteome.
SEQUENCE 307 AA; 33681 MW; E8BB622AE0C5C92C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  .68
                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 OSTLEORGFVGCARHFIECVONOTVPOTAGE 288
            DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 SGSLENVPNVGVNKNIFLKDQNIFVQKLLGQ
                                                                                                                                                                                                                   EcoGene: EG13879; mvim.
EcoGene: EG13879; mvim.
InterPro; IPR000668; GPC_IDH_MocA.
Pfam; PF01408; GFC_IDH_MocA.C.
Pfam; PF01408; GFC_IDH_MocA.C.
Pfam; PF02894; GFO_IDH_MocA.C.; 1.
                                                                                                                                                                                                         EMBL; AE000207; AAC74152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKEDQYMKMTVCLETEKKSP---
                                                                                                                                                                                                                                                                                                                                                                                                 20.78;
                                                                                                                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
corresponding to the 12. DNA Res. 3:137-155(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DHP dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AEQKGKVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NMH102-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid PHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHT4_PSEPU
Q05184;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
PHT4_PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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9;

3;

Gaps

19;

50; Indels

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36; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-92 FROM N.A.
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis,
                                                                                                                                                                                                                                                     YISS_BACSU
P40332; 007924;
                                                                                                                                                                            117 IVGH 120
                                                                                                                                               122 HEEH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
 Matches
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                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                    HAESTARLRLGVVGLGRAFTLMLPTFLADRR-----VQLVGACDPREQARRQFERDF 56
                                                                                                                                                                                                                                                                                                                                        2 NAEPERKFGVVVVGVGRAGSVR----MRDLRNPHPSSAFLNLIGFVSRRELG-----SI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1-carboxy-3-chloro-3,4-dihydroxycyclo hexa-1,5-diene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-97464069; PubMed-9322766.
Nakatsu C.H., Providenti M., Wyndham R.C.;
"The cis-diol dehydrogenase cbac gene of Tn5271 is required for growth on 3-chlorobenzoate but not 3,4-dichlorobenzoate."; Gene 196:209-218(1997).
                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                  DGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSL 104
                                                                                                                                                                                                                                                                                                                                                                                                                              57 DAPAYETIEDLAADSNVDALYIASPHQFHAEHTRIAAANRKHVLVEKPMALSL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 397;
                                                                                                                                                                                                                                                                                DB 1; Length 410;
                                                                                                                                                           EMBL; D13229; BAA02512.1; ...
InterPro; IPR000683; GFO_IDH_MOCA_C.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA, 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
Plasmid: Oxidoreductase; Aromatic hydrocarbons catabolism.
SEQUENCE 410 Aa; 45644 MW; 0D1A95B019DCACIA CRC64;
SIMILARITY: TO ALCALIGENES SP. 1-CARBOXY-3-CHLORO-3,4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BR60 / ISOLATE BLOODY RUN CREEK; TRANSPOSON-TN5271;
                                                                                                                                                                                                                                                                                                           46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA_C; 1.
Pfam; PF028044; GFO_IDH_MOCA_C; 1.
Oxidoreductase; Aromatic hydrocarbons catabolism.
SEQUENCE 397 AA; 44090 MW; EAD6115ECD61C042 CRC64;
             DIHYDROXYCYCLOHEXA-1,5-DIENE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 103.5; DI
Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 AA
                                                                                                                                                                                                                                                                                               0.8;
                                                                                                                                                                                                                                                                                              ; Pred. No. 0.8; 15; Mismatches
                                                                                                                                                                                                                                                                              6.9%; Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: TO P. PUTIDA PHT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%;
                                                                                                                                                                                                                                                                                              30.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U18133; AAC45718.1; -
                                                                                                                                                                                                                                                                              Query Match 6.9%
Best Local Similarity 30.1%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=285;
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Q44258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBAC_COMTE
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                                                                                                                                                                     57 LCKNPDVEVVYIGTPHQFHAVHABIALNAGKHVLVEKPMAVTLEDCCRMNACAQRAGKYL 116
                                                                                                                               ALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVL 121
13 VVGVGRA-----GSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLED 61
                                                              5 VVGLGKAFMLMLPTFLMDRRVQLVAASDTDP----LSLRQFKADFPAAAVHG----DIES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98015416; PubMed-9353932;
Roche B., Autret S., Medina N., Levine A., Vannier F., Seror S.J.;
A Bacillus subtilis chromosome segment at the 100 degrees to 102
degrees position encoding 11 membrane proteins.";
Microbiology 143:3309-3312(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oudega B., Koningstein G., Duesterhoeft A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01408; GFO_IDH_MOCA; 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
Hypothetical protein; Oxidoreductase; Complete proteome. SEQUENCE 342 AA, 37483 MW; B6DF205F9E4B0103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
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Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase yisS (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 AA
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Subtilist; Bd11065; yisS.
InterPro: IPR000683; GFO_IDH_MOGA.
InterPro: IPR004104; GFO_IDH_MOGA_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAB07962.1; -. -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z93940; CAB07962.1; -. EMBL; L08822; -; NOT_ANNOTATF EMBL; Z99109; CAB12924.1; -.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Rasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
Sampel G., Sexi Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                          E--DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK 117
                                                                                                          Gaps
                                                                  ERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFL----NLIGFVSR--RELGSIDGVQQISL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1657.
STRAIN-KIZ. / MG1657.
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDGJ OR B1624.
Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
20;
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-!- SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein; Oxidoreductase; Complete proteome. 346 AA; 38257 MW; 30F1E436EAC4F3CC CRC64;
                                                                                                                                                                                                                                                                                                                                                  118 GKVLHEEHVELLMEEFAFLKKEV----VGKDL-LKGSLLFTSD 155
                                                                                                                                                                                                                                                                                                                                                                                                                        GVICQVGFMRRFDPAYADAKRRIDAGEIGKPIYYKG---FTRD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase ydgJ (EC 1.-.-).
Mismatches
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EMBL; D90805; BAA15375.1; ALT_INIT.
EMBL; D90806; BAA15382.1; ALT_INIT.
EMBL; D90807; BAA15389.1; ALT_INIT.
EMBL; D90808; BAA15412.1; ALT_INIT.
ECOGENE; EC13931; ydgJ.
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InterPro; IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
32;
41; Conservative
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P77376;
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9
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Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: SOME, TO THE YHHX FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PLPVGVAENWLYLPCIKIAKEQIEKIGPVVAFTHNS-TGPFVTQNKYLTTTWRQKPEHIG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 RWDSDFLTLKGLLAEGVLGEVAYFESHFDRFRPQVRDRWREQGGPG-SGIWYDLAPHLLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 SLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 NLDEILNDPHVDYIDALLPAQFNADIVEKAVKAGKPVILEKPIAANLDQAKEIVKIAEST 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 GK------VLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRF- 162
                                                                            68 VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHEEHVE 127
                                                                                                  128 LLMEEFAFLK-----KEVVGKDLLKGSLLFTSDPLEEDRF---GFPAFSGI-----SRLT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 38.2 Kba protein in PRE5-FET4 intergenic region.
TRR315W OR YM9924.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 349;
  DB 1; Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 protein.
349 AA; 38215 MW; 77C7F72321BCAD1F CRC64;
6.8%; Score 103; DB 1
30.7%; Pred. No. 0.77;
iive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 KGPGLKRNRYLSFHFKSGSLENVPNVGVNKNIFLK 253
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                                                                                                                                                                                                                                                                                                                                                                        349 AA
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InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
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Pfam; PF02894; GFO_IDH_MOCA_C; 1.
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Matches 46; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                  Best Local Similarity
Matches 39; Conserv
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                                                                                                                                                                                                                                                                          184 QAITLFG 190
                                                                                                                                                                                                                                   175 WLVSLFG 181
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SEQUENCE 34
                                                                                                                                                                                                                                                                                                                                                                      YM94_YEAST
004869:
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    Query Match
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                                                                                                                                                                                                                                                                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure 4:1413-1428(1996).
-!- CATALYTIC ACTIVITY: D-glucose + D-fructose = D-gluconolactone + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucitol.
-!- COFACTOR: CONTAINS ONE TIGHTLY-BOUND NADP(H) MOLECULE PER SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loos H., Sahm H., Sprenger G.A.; "Glucose-fructose oxidoreductase, a periplasmic enzyme of Zymomonas mobilis, is active in its precursor form."; FEMS Microbiol. Lett. 107:293-298(1993).
                                                                                                                                                                                                                                                                                                                                                               Kanagasundaram V., Scopes R.K.; Cloning, sequence analysis, and expression of the structural gene encoding glucose-fructose oxidoreductase from Zymomonas mobilis."; Bacteriol. 174:1439-1447(1992).
                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose--fructose oxidoreductase precursor (EC 1.1.99.28) (GFOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-97148336; Pubmed-8994968;
Kingston R.L., Scopes R.K., Baker E.N.;
"The structure of glucose-fructose oxidoreductase from Zymomonas
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUCOSE--FRUCTOSE OXIDOREDUCTASE.
L -> Q (IN REF. 2; AA SEQUENCE).
C1E4A19F5B34267A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 101.5; DB 1; Length 439; 25.9%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mobilis: an osmoprótective periplasmic enzyme containing non-
dissociable NADP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-71 FROM N.A., AND SEQUENCE OF 2-16 AND 53-71.
STRAIN-ATCC 29191 / ZM6, AND ATCC 31821 / ZM4 / CP4;
MEDLINE-93231476; PubMed-8472911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01408; GFO_IDH_MocA; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
Oxidoreductase; NADP; Signal; Periplasmic; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- PATHWAY: SORBITOL-GLUCONATE PATHWAY.
-i- SUBUNIT: HOMOTETRAMEN.
-i- SUBCLLULAR LOCATION: Periplasmic.
-i- SUBCLLULAR ELOCATION: PERIPLAMENTY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
-----KNKEVIGSFTYGSAFG----ATEKSVFLK 250
                                                                                                                                                                                                                                                                                                            53-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M97379; AAA27690.1; -.
EMBL, X73088; CAA51534.1; -.
PDB; 1OFG, 21-ARP-9.
InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 29191 / ZM6;
MEDLINE-92165717; PubMed=1537789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47801 MW;
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                     Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                      NCBI_TaxID=542;
                                                                                        GFO_ZYMMO
007982:
                                                                                                                                                                                                                                                         2ymomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
226
                                                                      GFO_ZYMMO
qq
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Gaps

39;

Indels

45;

Conservative 19; Mismatches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller L.P., Crawford J.T., Shinnick T.M.;
"The rpoB gene of Mycobacterium tuberculosis.";
Antimicrob. Agents Chemother. 38:805-811(1994).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White V.,
Feterson J., DeBoy R., Bould M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Δ.
                                                                              --- DGVQQISLED-----ALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTL 102
                                                                                                     s:
                                      ----LNQILPGFAGCQHSRMKLWSAVTEKAKIV 124
51
                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98255987; PubMed=9634230; Garnier T., Churcher C., Harris I Cordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Rown D., Chillingworth T., Connor R., Badcock K., Basham D., Rown D., Chillingworth T., Murphy T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RNA)(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
6 ERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLI--GFV----SRRELGSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94304130; PubMed=8031050;
                                                                                                                                                               103 SLAAAQELWELAEQKGKVL 121
                                                                                                                                                                                      |:| | : : |: | 1
185 SVADCQRMIDAAKAANKKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-148 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 393:537-544(1998).
                                      81 DRRFGYAIVGLGKYA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bishai W.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : | | : | | | | | : | 1078 DKISKRQRLRV-----FKHEDGSERVLSDGDHVEVGQQLAMEGSADPHEVLRVQGPREV 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1019 GVGEDITGGLPRVQELFEARVPRCKAPIADVTGRV-RLEDGERFYKITIVPDDGGEEVVY 1077
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%; Score 100.5; DB 1; Length 1316; Best Local Similarity 21.2%; Pred. No. 6.7; Matches 62; Conservative 54; Mismatches 93; Indels 83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 EDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHV -----LVEYPMTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 SLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVV----GKDLLKGSLLFTSDPLE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 EDR------FGFPAFSGISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GVGR---AGSVRMRDL---RNPHPSSAFLNLIGFVSRRELGS------IDGVQQISL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 KKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVNKNIFLKDQNIFVQ 260
                                                                                                                                                                               Tuberculist; Rv668; -.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF001854; RNA_pol_A2; 1.
Pransferase; DNN-directed RNA polymerase; Transcription; COmplete proteome.
COmplete Froteome.
COMPLICT 594 594 G -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                            CONPLICT 594 594 G -> E (IN REF. 2).
SEQUENCE 1316 AA; 146769 MW; 45BF24839AF53E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 1, 2002, 14:47:42 Job time: 18.2283 secs
                                                                                                   EMBL; 295972; CAB09389.1; --
EMBL; AE006964; AAK44922.1; --
EMBL; L27989; AAA21417.1; --
TIGR; MT0696; --
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us-09-606-129a-1.rpr

Page 1

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:43:58; Search time 31.4084 Seconds (without alignments) 905.569 Million cell updates/sec Run on:

US-09-606-129A-1 1508 1 MNAEPERKEGVVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	biliverdin reducta	dehydrogenase, pro		probable oxidoredu	probable regulator	probable regulator		hypothetical prote			oxidoreductase hom	lipopolysaccharide	probable inositol	oxidoreductase ypj	se	hypothetical oxido	hypothetical prote	oxidoreductases ho	hypothetical prote	oxidoreductase hom	oxidoreductase hom	hypothetical prote	hypothetical prote	oxidoreductase hom	oxidoreductase (EC				
SUMMARIES	ΩI	S62624	G02066	A42268	AF2324	S74645	F90486	C65140	AH0994	A91165	A86011	н69216	D69803	AE2337	S75555	AE1119	B72359	. A71443	B86819	T39296	T38428	T42744	A11428	AC2319	AH1470	~	F89784	D71201	AF1109	AE3650
	DB	7	~	7	7	7	7	7	7	7	~	Н	7	7	7	7	7	7	7	7	7	~	~	~	7	~	7	Н	~	7
	Length		296	295	322	328	371	345	345	345	345	318	393	374	371	338	360	364	324	368	369	352	343	356	323	338	346	371	323	324
æ	Query	8	98.8	CA	14.7	4	0	٥.	•	•	9.8	•	•				•	8.8		•	•	8.3	•	•				8.1		7.9
	Score		1490	1245.5	221.5	218.5	155.5	152.5	150.5	œ.	œ.	142	139		134	3	133	132.5	131.5	128.5	128.5	125.5	124	123		122		121.5	о О	119.5
	Result No.		8	က	4	ស	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

δy g δ

241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296

NADH-dependent dyh	conserved hypothet	hypothetical prote	oxidoreductase (EC	oxidoreductases ho	oxidoreductase hom	oxidoreductase hom	dehydrogenase Atul	conserved hypothet	myo-inositol 2-deh	myo-inositol 2-deh	D-galactose 1-dehy	conserved hypothet	oxidoreductase ysj	oxidoreductase hom	oxidoreductase hom
A75025	G70026	T46531	AF3425	AH1802	AC1345	AF1715	AH2713	H70014	D98236	AG3049	E97495	A83004	G86852	AB1715	AG1344
7	7	~	r	7	7	7	7	~	7	7	7	7	N	0	7
341	358	342	390	343	358	358	308	328	330	330	334	360	305	349	349
7.9	7.9	7.7	7.7	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5	7.5
119	118.5	116.5	116.5	116	115	115	114.5	114.5	114.5	114.5	114.5	114	113.5	113.5	113.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1	
	S62624	
	biliverdin reductase (EC 1.3.1.24) - human	
	N.Alternate names: Diliverdin IX-alpha reductase	
	C:Date: 28-Oct-1996 #sequence revision 09-May-1997 #text change 21-Jul-2000	L-Jul-2000
	C; Accession: S62624; S62622; S29736	
	R; Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.	
	Eur. J. Biochem. 235, 372-381, 1996	
	A:TILLE: HUMAN DIIIVETONI 17-42pna reductase is a zinc-metalloprotein. Characterizati	Jein. Characterizati
	A; Accession: S62624	
	A; Molecule type: mRNA	
	A; Residues: 1-296 <mai></mai>	
_	A;Cross-references: EMBL:X93086; NID:91246748; PIDN:CAA63635.1; PID:91246749	LD:91246749
	A; Accession: S62622	
	A) MOLECULE LYPE: DECELOR 170 101-36.18-71.008-034.035-018 - MAES	
	R.Maines, M.D.: Trakshel, G.M.	
	Arch. Biochem. Biophys. 300, 320-326, 1993	
	A; Title: Purification and characterization of human biliverdin reductase.	ductase.
	A; Reference number: S29736; MUID:93143333	
	A; Accession: S29736	
	A; Molecule type: protein	
	A.Note: the sequence of mentide I from made 333 seems not to helona	na to this protein
	C. Ganation.	
	A; Gene: BVR	
	C;Keywords: oxidoreductase	
	F;3-296/Product: biliverdin reductase IX-alpha #status experimental	al <mat></mat>
	Query Match 100.0%; Score 1508; DB 2; Length 296;	
	Best Local Similarity 100.0%; Pred. No. 1.2e-109; Matches 296; Conservative 0; Mismatches 0; Indels 0;	0; Gaps 0;
	QY 1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE	DISLE 60
	Db 1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE	11111 DISLE 60
	Ţ	
	Qy 61 DALSSQEVEVAYICSESSSHEDYIRQFENAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120	2KGKV 120
	Db 61 DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWTLSLAAAQELWELAEQKGKV 120	2KGKV 120
	Qy 121 LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLF	LVSLF 180
	Dh 121 THERHVELTMENDARTKENVCKNILKGGTERFADERGEDARGGEDARGGETGRETHE	 
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A;Cross-references: GB:BA000019; PIDN:BAB75848.1; PID:g17133284; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                    54 L----VEREDIDLVVICTINRDHGAIARAALTAGKHVIVEYPLSVDLTEAEELIALAKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 ISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ENVP-NVGVNKNIFLKDON 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S74645
Bliverdin reductase (EC 1.3.1.24) - Synechocystis sp. (strain PCC 6803)
N;Alternate names: hypothetical protein slr1784
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                     DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV
                                                                                                                                        181 GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 KGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLF----TSDP-----LEEDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VVGVGRAGSVRMRDLRNPHPSSAFL----NLIG-----FVSRRELGSIDGVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 QQKLLHVEHIELLGGLHQALK ----QNLDKVGHLFYVRYSTINPQNPAPRKWTYNHAMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 GFPAFSGISRLTWLVSLFGELSLVSATLEERK---EDQYMKMTVCLETEKKSPLSW----
                                                                                                                                                                                                                             241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 322;
                                                                                                                                                                                                                                                                                                                              biliverdin reductase [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 221.5; DB Pred. No. 1e-09; 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IEEKGPGL-KRNRYLSFHFKSGSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                C; Species: Anabaena sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-322 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-322 <KU
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Best Local S:
Matches 87,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: bvdR
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                                                                                                                                      Species: Homo sapiens (man)
Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A42268
biliverdin reductase (EC 1.3.1.24) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A;Molecule type: nucleic acid; protein
A;Residues: 1-295 <FAK>
A;Cross-references: GB:M81681; NID:9203177; PIDN:AAA40830.1; PID:9203178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: A42268
R;Fakhrai, H.; Maines, M.D.
J. Biol. Chem. 267, 4023-4029, 1992
A;Title: Expression and characterization of a cDNA for rat kidney A;Reference number: A42268; MUID:92156147
A;Accession: A42268
                                                                                                                                                                                                                                                                                                                                                               Length 296;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                         A;Residues: 1-296 <KOM>
A;Cross-references: EMBL:U34877; NID:g1143231; PID:g1143232
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracted from NCBI backbone (NCBIP:82800)
                                                                                                                                                                                         T.; Tomita,
                                                                                                                                                                                                                                                                                                                                                          Score 1490; DB 2;
Pred. No. 3e-108;
2; Mismatches 2;
                                                                                                                                                                                                                     A;Reference number: H00768
A;Accession: G02066
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                 biliverdin reductase (EC 1.3.1.24) - human N;Alternate names: biliverdin IX-alpha reductase C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1996;Accession: G02066 R;Komuro, A.; Tobe, T.; Nakano, Y.; Yamaguchi, T.submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                                                                                                                                                            98.88;
98.68;
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Best Local Simi
Matches 292;
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Best Local
               241
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                                                                    RESULT 2
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215

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C; Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH0994
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Church
th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farr
S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 29-Sep-1999
C;Accession: C65140
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-345 <BLAT>
A;Residues: 1-345 <BLAT>
A;Cross-references: GB:AE000420; GB:U00096; NID:g1789840; PIDN:AAC76465.1; PID:g17898
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical 38.8 kD protein in gntR-ggt intergenic region - Escherichia coli (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSD------PLEEDRFGFP---AF-- 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|: :| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
           DALSSOEVEVAYICSESSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK---
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; Pred. No. 0.00025;
27; Mismatches 52;
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C;Superfamily: conserved hypothetical protein b1624
                                                                                                                                                                -GKVLHEEHVELLMEEFAFLKKEVVGKDL-----
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ilarity 31.3%;
Conservative 27
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Best Local Similarity
Matches 42; Conserv
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G:Species: Sulfolobus solfataricus
G:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequenc_revision 24-May-2001
C:Accession: F90486
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A.Description: Sulfolobus solfataricus complete genome.
A.Accession: F90486
A.Accession: F90486
A.Status: preliminary
A.Mocloule type: DNA
A.Residues: 1-371 <KUR>
A.Residues: 1-371 <KUR
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74645
K;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                           A; Reference number: S74322; MUID:97061201
A; Reference number: S74322; MUID:97061201
A; Accession: S74645
A; Accession: S74645
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-128 «KAN>
A; Residues: 1-128 «KAN>
A; Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAA16797.1; PID:d101753
C; Keywords: oxidoreductase
                                                                                                                                                                                           A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGKVLHEEHVELLMEEFAFLKKEV--VGKDL-LKGSLLFTSDPLEE-----DRFGFPAF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGISRLTWLVSLFGELSLVSATLE--ERKEDQYMK---MTVCLETEKKSPLSWIEEKGPG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 LKRN-RYLSFHFKSGSL------ENVPNVGVNKNIFLKDQNIFVQKLLGQFS 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ATPVR----VGIVGTGYAAQRRAEVFRGDRRS-----QLVSFWGNSEANTAKFADTFGVRPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSR-----RELGSIDGV-QQISLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%; Score 218.5; DB 2; Length 328; 25.2%; Pred. No. 1.8e-09; tive 57; Mismatches 141; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 EKELAAEKKRILHCLGLAEEIQKYC 292
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66; Conserv
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Matches
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enterohemorrhagic Escherichia coli 0157:H7
MUID:21074935; PMID:11206551
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A; Title: Genome sequence of A; Reference number: A85480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                          A; Residues: 1-345 <STO>
                                          A, Accession: A86011
A, Status: preliminary
A, Molecule type: DNA
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
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                                                                      A; Cross-references: GB: AL513382; PIDN: CAD08084.1; PID: 916505063; GSPDB: GN00176 C; Genetics:
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: A91165
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                                                                                                                                                                                          10.0%; Score 150.5; DB 2; 32.6%; Pred. No. 0.00036; tive 25; Mismatches 55;
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                                                                                                                            A;Gene: STY4266
C;Superfamily: conserved hypothetical protein b1624
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                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <PAR>
                                                                                                                                                                                                             Similarity
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A; Accession: AH0994
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Best Local S
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3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein - Methanobacterium the G.Specias: Methanobacterium thermoautotrophicum (C.Specias: Methanobacterium thermoautotrophicum (C.Specias: Methanobacterium thermoautotrophicum (C.Specias: Methanobacterium thermoautotrophicum (C.Specias: Methanobacterium theory) (C.Specias: Methanobacterium theory) (C.Specias: Methanobacterium theory) (C.Specias: Methanobacterium thermoautotrophicum Delta H: Methanobacterium thermoautotrophicum Delta H: fun A; Reference number: A69000; MUID:98037514 (Methanobacterium thermoautotrophicum Delta H: fun A; Reterence number: A69000; MUID:98037514 (Methanobacterium thermoautotrophicum Delta H: fun A; Reterence number: A69000; Muid: Assetum thermoautotrophicum Delta H: fun A; Reterence number: A69000; Muid: Assetum thermoautotrophicum Delta H: fun A; Reterence number: A69000; Muid: Assetum thermoautotrophicum Delta H: fun A; Reterence number: A69000; Muid: Assetum thermoautotrophicum Delta H: fun A; Molecule type: DNA...
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121 GHVERFNPAVQKAKELIENDVIG-DVVSASAKRVGPFPPRIKDVGVTIDLAIHDLDVMHY 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFTSDPLEE-----VSLFGE 182
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 142; DB 1; Length 318
Pred. No. 0.0015;
0: Mismatches 96; Indels
                                                                                                                                                                                                               Query Match 9.8%; Score 148.5; DB 2; Best Local Similarity 30.6%; Pred. No. 0.00052; Matches 41; Conservative 27; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50; Mismatches
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QΩ

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hypothetical protein s110816 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S75555
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-371 <KNA
A; Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18116.1; PID:g165
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: Streptomyces griseus stri protein
                        A;Molecule type: DNA
A;Residues: 1-374 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75951.1; PID:917133387; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a114252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EVQVIPDFEFRFVPAWQYVAELLGGGILGOLKLIKVDWLVGSRANPNRAWNWYAQREK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 EDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWTLSLAAAQELWELAEQKGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IATVDF-----EFRFVPAWQLFAELLSS-------GYVGTPRLIRIDWLGSS 165
                                                                                                                                                                                                                                                                                                                                                   8 KFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQI-----SL 59
                                                                                                                                                                                                                                                                                                                                                                                        11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQI-----SLEDA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 VAVIGTGFGQAVHIPALQYHQQTQAIA----IYHRDLAKAQEVAKSNDLAYSYNNLEEL 63
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                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 EEHVELLME-EFAFLK-----KEVVGKDLLKGSLLFTSDPLEEDR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----RPWNWYSSKEKGGG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 FGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWI--EEKGPG
                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                  Score 136.5; DB 2;
Pred. No. 0.0049;
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                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S74322; MUID:97061201
A;Accession: S75555
                                                                                                                                                                                                         9.1%; Scu.
21.8%; Pred
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23.2%;
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                          Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                           Cypecies: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: D69803
R;Kunst, F: Ogasawara, N: Moszer, I:;Albertini, A.M.;Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Febret, C.; Ferrari, E.
Alathors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler,
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsapel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Ladinois,
Alathors: Lauber, J.; Lazarevic, V.; Eece, S.M.; Sadaie, Y.; Sato, T.; Sconfone,
M;Authors: Lauber, J.; Lazarevic, V.; Eece, S.M.; Sadaie, Y.; Sato, T.; Seronion,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquei, J.; Sekowska, A.; Seronion,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Voshkawa, H.F.; Zumstein, E.; Yoshkawa, H.; Danchin, A.
A;Ttle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: D69803
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-393 <a href="https://doi.org/10.1016/j.nl.">https://doi.org/10.1016/j.nl.</a>
A;Gene: yfil
A;Gene: yfil
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K; Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, W.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKISAAQKWRVDPAIAGPS-----FVLGDLS------THTYYMSQLIMPKMKIKEL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 139; DB 2; Length 39
Best Local Similarity 23.3%; Pred. No. 0.0034;
Matches 65; Conservative 51; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L----SWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVN 247
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                        238
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5
                                                                                                                                 Query Match 8.8%; Score 133; DB 2; Length 338;
Best Local Similarity 30.3%; Pred. No. 0.0081;
Matches 30; Conservative 26; Mismatches 31; Indels 12; Gaps
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Search completed: November 1, 2002, 14:50:54 Job time: 33.575 secs

Sequence 1, Appl1
Sequence 1, Appl1
Sequence 69, Appl
Sequence 112, App
Sequence 69, Appl
Sequence 2, Appl1
Sequence 2, Appl1
Sequence 10, Appl
Sequence 2, Appl1
Sequence 3, Appl1
Sequence 3, Appl1

US-07-992-827D-1 US-08-216-593-1 US-08-81-843A-69 US-08-974-549A-112 US-08-974-549A-112 US-09-430-323-69 US-09-430-323-69 US-09-641-782-6 US-09-541-782-10 US-09-541-782-2 US-09-141-822-2 US-09-141-822-2 US-09-147-809-2 US-08-960-780-44 US-08-950-780-44

323 323 323 323 323 988 988 988 1261 1057 1073 472 2930 835 835 833 333 333 333 333

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(without alignments)
292.168 Million cell updates/sec
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1508
1 MNAEPERKFGVVVVGVGRAG.....RILHCLGLAEEIQKYCCSRK
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB:
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                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database

7)

### Sequence 3, Appli Sequence 6, Appli Sequence 1, Appli Sequence 519, Appl Sequence 15, Appl Sequence 15, Appl 19, Appl 19, Appl 2, Appl 15, Appl 11, Sequence 15, No Sequence 19, No Sequence 2, No Sequence 2, No Sequence 2, No Sequence 11, No Sequence 11, No Sequence 14, No Sequence 2, No S Description US-09-720-811-6 US-09-720-811-6 US-09-720-811-1 US-09-036-198A-15-1 US-08-308-198-19 US-08-308-198-19 US-08-402-217A-2 US-08-995-654-2 US-08-995-654-2 US-08-995-654-1 US-08-111-44-8 US-08-111-44-8 US-08-111-44-8 US-08-111-44-8 US-08-960-022-14 PCT-US95-16311-1 US-09-330-330-1 r-US95-16311-2 -09-720-817-3 US-08-372-652-2 -08-372-652-1 SUMMARIES 8 4061166211126642666 % Query Match Length E WWH2HHR8000088777 124.5 124.5 122.5 108 107 107 98 900 900 900 888 87 886 848 848 848 83.5 8228 8228 8228 8228 Result Š

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ALIGNMENTS	RESULT 1 US-09-720-817-3 Sequence 3, Application US/09720817 Sequence 3, Application US/09720817 Sequence 3, Application US/09720817 Settent No. 6346579 GENERAL INFORMATION: APPLICANT: Masai, Eiji APPLICANT: Katayama, Yoshihiro APPLICANT: Katayama, Yoshihiro APPLICANT: Mishikawa, Seiji APPLICANT: Mishikawa, Seiji APPLICANT: Mishikawa, Seiji APPLICANT: Moshikawa, Seiji APPLICANT: Jose 1009660SOXPCT CURRENT ELING DATE: 2009660SOXPCT CURRENT APPLICATION NUMBER: JAPAN 10/203200 PRIOR APPLICATION NUMBER: JAPAN 10/203200 PRIOR APPLICATION NUMBER: PCT/JP99/03410 PRIOR APPLICATION NUMBER: PCT/JP99/03410 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 315 TYPE: PRT CORGANISM: Sphingomonas sp. CR-0310201	Query Match 8.3%; Score 124.5; DB 4; Length 315; Best Local Similarity 20.4%; Pred. No. 7.2e-05; Matches 65; Conservative 55; Mismatches 147; Indels 51; Gaps	QY 11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDAL 63 ::	Qy 64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELMELAEQKGKVLHE 123 : 1: 1: 1   1   1   1   1   1   1   1	QY 124 EHVELLMEEFAFLKKEVVGKDL

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Gaps

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64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 122.5; DB 4
22.5%; Pred. No. 9.7e-05;
Live 33; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: SmithKline Beecham Corporation 709 Swedeland Road
CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: JAPAN 10/203200

PRIOR FILING DATE: 1998-07-17

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 280
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FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Sphingomonas sp. CR-0310201
PUBLICATION INFORMATION:
US-09-720-817-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 519, Application US/08936165A Patent No. 6348582
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FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 EHVELLMEEFAFLKKEVVGKDL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 GHTRRFNPSHQYIHNKIVAGEL 140
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.54
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodgson, John
Knowles, David
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CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Black,
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ZIP: 19406-0939
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LKGS-----LLFTSDPLE 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 VDLFAYQAGKIVQANAVQGPIHPELGIAMDMSIQLKSETGAICTLSLSFNNDGPLGTFFR 238
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FUKUGA MASSAO

APPLICANT: FUKUGA MASSAO

APPLICANT: FUKUGA MASSAO

APPLICANT: MISHIAWA SELJI

APPLICANT: MISHIAWA SELJI

APPLICANT: HOLTA YASUSHI

TITLE OF INVENTION: NOVEL GENE AND TRANSFORMANT CARRING THE SAME

TITLE OF INVENTION: NOVEL GENE AND TRANSFORMANT CARRING THE SAME

FILE REFERENCE: 2009660SOXPCT

CURRENT APPLICATION NUMBER: US/09/720,817

CURRENT FILING DATE: 1998-00-17

PRIOR FILING DATE: 1998-00-17

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 315
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APPLICANT: Fukuda, Masao
APPLICANT: Katayama, Yoshihiro
APPLICANT: Katayama, Yoshihiro
APPLICANT: Hotta, Yasushi
TITLE OF INVENTION: NOVEL GENE AND TRANSFORMANT CARRYING THE SAME
STIE REFERENCE: 20096GHOSOXPCT
CURRENT APPLICATION NUMBER: US/09/7120,817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124.5; DB 4 Pred. No. 7.2e-05;
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US-09-720-817-6
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                                                                                                                                                                                                                                Sequence 6, Application US/09720817
Patent No. 6340579
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Patent No. 6340579
GENERAL INFORMATION:
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      272 AAEKKRILHCLGLAEEIQ 289
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295 A----RVLDCYRVLGELE 308
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A----RVLDCYRVLGELE 308
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                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Masai, Eiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
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153 TSDPLEEDRFGFPAFSGISRLTWL-----VSLFGELSLVSATLEERKEDQY-MKMT 202
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                                                                                                                                                                                                                                                 102 ISLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKG-----SLLF 152
                                                                                                                                                                                                                                                                          153 TSDPLEEDRFGFPAFSGISRLTWL-----VSLFGELSLVSATLEERKEDQY-MKMT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 FAARFECEAVLGYORL----LERPDIDAVYVPLPPGMHAEWIGKALEADKHVLAEKPLT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 LSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKG-----SLLF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 FVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMT 101
                                                                                                                                                          42 FVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bartz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Adduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US 09/36987
EARLIER APPLICATION NUMBER: US 09/36987
SARLIER APPLICATION NUMBER: US 09/36987
SARLIER FILING DATE: 1998-08-09
NUMBER OF SEO ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.1%; Score 107; DB 4; Length 332; 23.1%; Pred. No. 0.0052; tive 36; Mismatches 77; Indels
                                                                     Length 332;
                                                                                                                77; Indels
                                                                     Score 107; DB 4;
Pred. No. 0.0052;
                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONCANISM: Saccharopolyspora spinosa US-09-370-700-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09370700 Patent. No. 6274350 GENERAL INFORMATION:
                                                              Query Match 7.1%;
Best Local Similarity 23.1%;
Matches 43; Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 23.1%
Matches 43; Conservative
    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 VLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |::|
215 VLLQSE 220
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                                                                                                                                                                                                                                                                                                                                                                                                                           203 VCLETE 208
           ; MOLECULE TIPE
US-09-036-987A-15
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US-08-286-819A-19
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US-09-370-700-15
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                                                                                                                                                                                                                                                                                                                                                                                  54 LKDDTIDVIHVCTPNDSHCEITVAGLHAGKHVWCEXPWAKTTAEAQKMIDTAKSTGKKLT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | : | | | 114 IGYQNRFRPDSQFLHQAAQRGDL--GDIYFGKAHAIRRRAVPTWGVFLNEEAQGGGPLID 171
                                                                                                                                                                                                                                                                                                                                                                                                                                              EEHVELLMEEFAFLKKEVVGKDLLKGSLLF-----TSDPL-----EEDRFGFPAFS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Broughton, Mary C.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Tradaday, Patti J.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADRESS:
Annercen
                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 IGTHALDLTLWMMDNYEPESVMGSTFHK------LNKOHDAPNAW 210
                                                                                                                                                                                                                                                                 7.2%; Score 10%; DB 4; Length 229; 22.2%; Pred. No. 0.0023; live 31; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUBER: US/09/036,987A FILING DATE: 09-MAR-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFRENCE/DOCKET NUMBER: 50,6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4816
                                                                  519:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                           INFORMATION FOR SEQ ID NO: 519
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPOLOGY: linear
MOLECULE TYPE: Protein
US-08-936-165A-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 332 amino acids amino acid
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.28
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BROUGHTO
APPLICANT: BROUGHTO
APPLICANT: Crawford
APPLICANT: Madduri,
APPLICANT: Merlo, DO
APPLICANT: Treadway
APPLICANT: Treadway
APPLICANT: Waldron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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US-09-036-987A-15
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APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: MOLINAS, CATHERINE
TITLE OF INVENTION: PARRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESSED OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
          246 VQISHLHRNRLLQLSRLGSRYEPYAFRDFQENKRYSILTIYLLQLTQELTDKAFEIHDRQ 305
                                                                                 ----LKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                            241 VPNVGVNKNIFLK--------DQN-----IFVQKLLGQFSEKELAAEKKR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA.
PPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                              196 DQYMKMTVCLETE----KKSPLSWIEEKGPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/174,682 FILING DATE: 28-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/917,146 FILING DATE: 10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08980357 Patent No. 6013508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Oblon, No. 6013508man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                          278 ILHCLG----LAEEIQK 290
                                                                                                                                                                                                                                                                                                                       ILSLLSKGRKAQEEIQK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-980-357-19
                              152 LRK---
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                                                                                                                                                                                                                                                                                                                          306
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                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERIUE
APPLICANT: OCURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: PRESPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
TITLE OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 LKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEERKE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 SVRMRDLRNP-----HPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICS 75
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 988;
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Best Local Similarity 20.8%; Pred. No. 0.24;
Matches 66; Conservative 50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patenth Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSILLAGIATOR 3-2
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-0CT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5871910man F.
REGISTRATION NUMBER: 24 4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 60-060-0 PCT FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION 0435
PRIOR APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
Sequence 19, Application US/08286819A
Patent No. 5871910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   988 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-286-819A-19
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124 LEEKYDSMVQSLEDVTAQFESYKALT----ASEIEDLKLENSSLQEKVAKAGKNAEDVQ 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 VQQISLE-DALSSQEVEVA----YICS-----ESSSHEDYIRQFLNAGKHVLVEYPM 100
                                                                                                                                                                                                                                                                                                                                                                                                          155 -----DPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEER------ 193
                                                                                                                   Gaps
                                                                                                                                                                                                                 97;
                                                      Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2. Application US/08700178
Patent No. 578369
Patent No. 1976
Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 VNKNIFLKDQNIFVQKLL----GQFSEKELAAEKKRILHCLGLAEEIQKY 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 -----LKQQEEDFRKQLEDEGGRKAEKENTTAE------LTEEINKW 262
                                                      ; Score 90.5; DB 1; Length 3; Pred. No. 0.3; 42; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0028-1 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,178
FILING DATE: August 20, 1996
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,217
FILING DATE: MARCH 10, 1995
ATTORNEY/AGENT INFORMATION:
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                                                      6.0%;
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amino acid
                                                                                                                Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                      Query Match
Best Local Similarity
Matches 68; Conserv
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US-08-402-217A-2
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US-08-700-178-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 VQISHLHRNRLLQLSRLGSRYEPYAFRDFQENKRYSILTIYLLQLTQELTDKAFEIHDRQ 305
                                                                                                                                                                                                                                                                     76 ESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEERKE 195
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                                                                                                                                                                                                                                21 SVRMRDLRNP-----HPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DQN-----IFVQKLLGQFSEKELAAEKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                             Query Match 6.5%; Score 98; DB 3; Length 988; Best Local Similarity 20.8%; Pred. No. 0.24; Matches 66; Conservative 50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,217A
FILING DATE: 10 MAR-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0155
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
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                        ; MOLECULE TYPE: protein US-08-980-357-19
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TOPOLOGY: linear
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54 VQQISLE-DALSSQEVEVA----YICS-----ESSSHEDYIRQFLNAGKHVLVEYPM 100
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                                                                                                                                                                                                                                                                                                                                                     -----KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVG 245
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                                                                                                                                                                                                                                                                    -----DPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEER------ 193
                                                                                                                                                                                     101 TLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGK--DLLKGSLLFTS---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Katz, Leonard
APPLICANT: Katz, Leonard
APPLICANT: Delcardayre, Stephen B.
APPLICANT: Davies, Julian E.
APPLICANT: Davies, Julian E.
TITLE OF INVENTION: COENZYME A DISULFIDE REDUCTASE,
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                6.0%; Score 90.5; DB 3; Length 351;
23.4%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 VNKNIFLKDQNIFVQKLL----GQFSEKELAAEKKRILHCLGLAEEIQKY 291
                                                             83; Indels
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                             42; Mismatches
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FILING DATE: 02-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08886886 Patent No. 6107068 GENERAL INFORMATION:
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TELEPHONE: 847-938-3137
                                          23.48;
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REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
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LENGTH: 551 amino acids
                                                             68; Conservative
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APPLICATION NUMBER:
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                                          Similarity
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US-08-886-886-15
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                       Query Match
                                            Best Local
                                                           Matches
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                                                                            54 VQQISLE-DALSSQEVEVA----YICS-----ESSSHEDYIRQFLNAGKHVLVEYPM 100
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                                                                                                                                                                                                                                             155 ----- DPLEEDRFGFPAFSGISRLTWLVSLFGELSLVSATLEER------ 193
                                                                                                                                                                                                                                                                                                                              -----KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVG 245
                                                                                                                                                                                                                                                                                                                                                     179 HQILATESSNQEYVRMLLDLQT--KSALKETEIK-----EITVSFLQKITDLQNQ---- 226
                                                                                                                                                              101 TLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGK--DLLKGSLLFTS---- 154
                                                                                                                                                                                                                                                                                     124 LEEKYDSMVOSLEDVTAQFESYKALT----ASEIEDLKLENSSLQEKVAKAGKNAEDVQ 178
                                          Gaps
                                                                                                      97;
6.0%; Score 90.5; DB 1; Length 351;
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APPLICANT: Wilde, Craig
APPLICANT: Wilde, Craig
APPLICANT: Solihamer, Jeffrey
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 -----LKQQEEDFRKQLEDEEGRKAEKENTTAE-----LTEEINKW 262
                                                                                                                                                                                                                                                                                                                                                                                                             246 VNKNIFLKDQNIFVQKLL----GQFSEKELAAEKKRILHCLGLAEEIQKY 291
                                        Indels
                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                   Pred. No. 0.3;
                                      42; Mismatches
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FILING DATE: December 22, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/700,178
FILING DATE: August 20, 1996
PRIOR APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
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; Sequence 2, Application US/08995654
; Patent No. 6025138
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TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                 23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                        68; Conservative
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                   Similarity
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Query Match
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                     Best Local
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                                    13;
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                                                                                                                                                                                                                                                                                                                    50 SIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTL----- 102
                                                                                                                                                                    103 -----SLAAAQELWELAEQKGKVLHEEHVELIMEEFA-----FLKKEVVGKDLLKGS 149
                                                                                                                                                                                                                                                                                             150 LLFTSDPLEEDRFGFPAFSGISRL-----TWLVSLFGELSLVSATLEERKEDQYMKMTV 203
                                      Gaps
                                                                      1 MNAEPERKFGVVVVGVGRAGSVRMRDLRN------PHPSSAFLNLIGFVSRRELG 49
                                    74;
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APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCE: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    204 CLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNV---GVNKNI 250
                                                                                                                                                                                                                                                                                                                                                                                             : | |: | |: | |: | 353 VIHVSGKDHASYYPEATDILLK---LIFHPETGEIYGAQGVGAKGVDKRI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: Switzerland
ZIP: (note: this is an international post code) CH-8092
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
DB 3; Length 551;
                                  42; Mismatches 110; Indels
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5.8%; Score 88;
22.1%; Pred. No.
                   Pred. No.
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AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: bovine FEATURE: Protein kinase; PUBLICATION INFORMATION:
                                    64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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DESCRIPTION: protein
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                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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VOLUME: 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                      9 FGVV-VVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67
                                                                                                                                                                                                                                                                                                                                                                               3 FNIIDTLGVGGFGRVELVQLKSEESKTFAMKIL---KRRHI---VDTRQQ----EHIRSEKQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 HVELLMEEFAFL-KKEVVGKDLLKGSLLFTSDPLEEDR-----FGFPAFSGISRLTW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 VRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHE 81
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                                                                                                                            Length 264;
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                                                                                                                                                                                                                      73; Indels
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86; DB 1;
Pred. No. 2.9;
                                                                                                                            Score 87; DB 2;
Pred. No. 0.45;
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                                                                                                                                                                                                                      33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UCB96-055
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REFERENCE/CDCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
TELEPAX: (415)343-4341
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 759 amino acids
TYPE: amino acids
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.7%;
Best Local Similarity 22.3%;
                                                                                                                            Query Match
Best Local Similarity 21.8%;
Matches 39; Conservative 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Conservative
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CITY: San Francisco
STATE: CA
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; DATE: 198
US-07-857-224B-9
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                                                                                                                  194 KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFH--FKSG--SLENVPNVGVN-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 DYIRQFLNAGKHVLVEYPMTLSL-AAAQELWELAEQKGK-----VLHEEHVELLMEEFA 134
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                                              -----AGGLKL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08676974

Patent No. 5770422

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: COLLINS, KATHLEEN

TITLE OF INVENTION: Human Telomerase

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Science & Technology Law Group

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFOCATION:
NAME: OSEMEN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELERAK: (415)343-4341
TELERAK: (415)343-4341
INFORMATION FOR SEQ ID NO: 1:
                                            382 QFMTQEAAQKCLLAAS-----PENE----
                                                                                                                                                                                                           |: ||||||| :
467 ERFELLKHQKLKDQNIFVSR 486
                                                                                                                                                                                  248 -----KNIFLKDQNIFVQK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                RESULT 15
US-08-676-974-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-676-974-1
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:40:53; Search time 67.0997 Seconds Run on:

(without alignments)
489.985 Million cell updates/sec

1508 1 MNAEPERKFGVVVVGVGRAG.....RILHCLGLAEEIQKYCCSRK 296 US-09-606-129A-1 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_032802:* Database :

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•				
Result		Ouery				
Q	Score	Match	Match Length DB	DB	ID	Description
1	225	14.9	09	21	AAG02024	Human secreted pro
7	186	12.3	63	21	AAG02023	Human secreted pro
m	152.5	10.1	434	22	ABG21584	Novel human diagno
4	148	9.6	241	22	ABG21582	Novel human diagno
2	148	9.8	389	22	ABG29497	Novel human diagno
9	129	8.6	335	22	ABB60024	Drosophila melanog
7	124.5	8.3	315	21	AAY68460	Sphindomonas sp. C
80	122.5	8.1	226	22	AAU49252	Propionibacterium
σ	122.5	8.1	280	21	AAY68459	Sphingomonas sp. C
10	121.5	8.1	175	18	AAW28328	Amino acid sequenc
11	120.5	8.0	337	22	AAG92054	C glutamicum prote

Corynebacterium gl Staphylococcus aur Putative P. abyssi	Staphylococcus aur Staphylococcus aur	Staphylococcus aur Glucose-fructose o	Streptomyces gal11	Micromonospora eve	SpnN protein invol	S. spinosa protein	Putative P. abyssi	Propionibacterium	E. coli growth and	Group B Streptococ	Novel human diagno	Mycobacter1um tube	Propionibacterium	Propionibacterium	H. pylori GHPO 138	Transposase from g	Human cancer assoc	Human male enhance	C glutamicum prote	Corynebacterium gl	Drosophila melanog	Streptococcus pneu	Putative P. abyssi	C glutamicum prote	Novel human diagno	C glutamicum prote	Corynebacterium gl		Staphylococcus aur
AAB79386 AAU36865 AAB96416	AAU34111 AAU34110	AAU36864 AAW77759	AAE00480	AAU04826	AAY39310	AAB70956	AAB96316	AAU43141	AAG98892	AAU03634	ABG20518	AAG81126	AAU49114	AAU56511	AAW98401	AAR24302	AAB43883	AAB69070	AAG93130	AAB79395	ABB67972	AAU37906	AAB96297	AAG89930	ABG24349	AAG89934	AAB79394	AAW01052	AAU34397
222	22	22 19	22	22	20	22	22	22	22	22	22	22	22	22	19	13	21	22	22	22	22	22	22	22	22	22	22	17	22
337 346 341	341	359 229	329	344	332	336	315	344	307	327	753	1316	702	413	219	988	424	1374	359	359	417	623	867	337	237	341	341	S	433
	7.7		7.2	7.2	7.1	7.1	7.1	7.1	7.0	7.0	9.8	6.7	6.5	6.5	6.4		6.4	6.4	6.3	6.3	6.2	6.2	6.1	0.9	0.9	0.9	0.9	0.9	0.9
120.5 119.5 119	116.5	110 108	108	108	107	107	106.5	106.5	105.5	105	102	100.5	98.5	97.5	6	46	96	96	95	95	94	93	92.5	9	0	90.5	0	90.5	90.5
12 13 14	15 16	17 18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

Human secreted protein, SEQ ID NO: 6105. AAG02024 standard; Protein; 60 AA. (first entry) 06-OCT-2000 AAG02024; AAG02024 

; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping. Human; 5' EST; gene therapy; c

Homo sapiens.

06-SEP-2000.

EP1033401-A2.

21-FEB-2000; 2000EP-0200610.

99US-0122487 26-FEB-1999;

(GEST ) GENSET.

Glordano J; Duclert A, Dumas Milne Edwards J,

WPI; 2000-500381/45. N-PSDB; AAC02030.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

forensic, gene therapy and

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RESULT
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                                                                   The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 225; DB 21; Length 60;
Pred. No. 2.2e-14;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRDLRNPHPSSAFLNLXGFVSRRELGSIDGVQQISLEDALSSQEVEV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 MRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A, Giordano J;
Claim 13; SEQ ID 6105; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID 6104; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein, SEQ ID NO: 6104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG02023 standard; Protein; 63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%;
97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The complex can gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and it is such as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insorties involving aberrant protein esquences have applications in the printed diagnostics, forensics, gene mapping, identification of mutations of mutations and produce other types of data and products dependent on DNA and mino acid sequences. ABG00010-ABG30377 represent novel human can amino acid sequence of data and products dependent on DNA and sugangostic anino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                           ö
                                                                                                                                                                           Gaps
DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy an chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                           ;
0
                                                                                                                                Length 63;
                                                                                                                                                                           Indels
                                                                                                                                                                           2;
                                                                                                                              Score 186; DB 21;
Pred. No. 1.4e-10;
0; Mismatches 2;
                                                                                                                                                                                                                      1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNL 39
                                                                                                                                                                                                                                               1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNXHPXSAFLNL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 51943; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #21575.
                                                                                                                                                                                                                                                                                                                                                                            ABG21584 standard; Protein; 434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                12.3%;
94.9%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                         37; Conservative
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                                                                                                                                                       Similarity
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                                                                                          63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS85771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                       ABG21584;
                                                                                          Sequence
                                                                                                                                Query Match
Best Local 8
                                                                                                                                                                           Matches
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us-09-606-129a-1.rag

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Local Similarity
                                                                                         241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS93684.
  for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2000;
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responsible
and to produ
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                                                                                                                                    43;
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                                                                                                                                    Matches
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                                                                    4 ;
                                                                                        59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                   119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSD-----PLEEDRFGFP---AF-- 167
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                    forensic;
                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic. food supplement; medical imaging; diagnostic; genetic disorder.
                                                                   13;
                                            Length 434;
                                                                   Indels
                                                                  52;
                                            DB 22;
                                            10.1%; Score 152.5; DB 2
31.3%; Pred. No. 3.5e-06;
ive 27; Mismatches 52
 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 51941; 103pp; English.
                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #21573.
                                                                                                                                                                                                                                                          ABG21582 standard; Protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
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2000US-0649167
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                                                                   Conservative
                                                                                                                                                                              SGISRLTWLVSLFG 181
                                                                                                                                                                                                   LGVHTMDQIISLFG 275
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                                                      Local Similarity
les 42; Conserv
                        434 AA;
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                       Sequence
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                                             Query Match
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genetic disorders or other traits to assess blodiversity
               and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 LDEVLNDPDVKLVVVCTHADSHFEYAKRALEAGKNVLVEKPFTPTLAQAKELFALAKSKG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSD-----PLEEDRFGFP---AFSG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                             Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                         9.8%; Score 148; DB 22;
29.9%; Pred. No. 4.3e-06;
tive 28; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #29488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : | : | : | : | 1.00 TELESTRADSS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 ISRL-----TWLVSLFGELS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG29497 standard; Protein; 389
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2000US-0649167
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cell-cell interactions in higher
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                          LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                         KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSD-----PLEEDRFGFP---AFSG 169
                                                                                                                                                                                                                                                                                                                 282 LTVTPYQNRRFDSCFLTAKKAIESGKL--GEIVEVESHFDYYRPVAETKPGLPODGAFYG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                     20;
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                                                                                                                                                                                           Length 389;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 6864
                                                                                                                                                                                           Score 148; DB 22;
Pred. No. 8.3e-06;
8; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                         ISRL-----TWLVSLFGELS 184
                                                                                                                                                                                                                                                                                                                                                                                                                        ABB60024 standard; Protein; 335
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                      389 AA;
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                                                                                                                                                                       Sequence
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid-eta-semialdehyde dehydrogenase (CHMSD) originating in
Sphingomonas sp. CR-0310201. CHMSD can be used in the production of
2-pyrone-4,6-dicarboxylic acid by culture of a transformant comprising
CHMSD in the presence of a suitable precursor such as
3,4-dihydroxybenzoic acid (which is converted in situ into
alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 GSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an alpha-hydroxy-gamma-carboxymuconic
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNAEPERKFGVVVVG-----VGRAGSVRMRDLRNPHPSSAFLNLIG-----FVSRREL- 48
insecticides, therapeutics and pharmaceutical drugs. The invention
                         discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MQSQANLNWGIAAAGRITQDFVTALGTVE----KSRHVVVAVADVDGQRAQQFAQRNQIP
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                                                                                                                                                                                                                                                                                                    Length 335;
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                                                                                                                                                                                                                                                                                                                                                                    62;
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                                                                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                                                    Query Match 8.6%; Score 129; DB 22
Best Local Similarity 27.7%; Pred. No. 0.00047
Matches 44; Conservative 28; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY68460 standard; Protein; 315 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP03410.
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                                                                                     (ABB57737-ABB72072)
                                                                                                                                                                                                                                              335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sphingomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200004134-A1.
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                                                                                                                                                                                                                                                 Sequence
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WPI; 2000-147784/13.
N-PSDB; AAZ88147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sphingomonas sp
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                                                                                                                                                                                                                                           48;
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                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                       72
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AAY68459
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                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthealmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                214
                                                                                                              119 GHTRRFNPSHQYIHNKIVAGELAIQQMDVQTYFFRRKNMNAKGEPRSWTDHLLWHHAAHT 178
                                                                                                                                                                                                  179 VDLFAYQAGKIVQANAVQGPIHPELGIAMDMSIQLKSETGAICTLSLSFNNDGPLGTFFR 238
                                                                                                                                                                                                                                    64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                        124 EHVELLMEEFAFLKKEVVGKDL-------LKGS-----LLFTSDPLE 158
                                         Gaps
                                                                       Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                         11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL 63
                                                                                                                                                                                                                       WIEEKGPGLKRNRYLSFHFKSGSLE--NVPNVGVNKN-IFLKDQNIFVQKLLGQFSEKEL
                                                                                                                                                                              159 EDRFGFPAFSGISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLS----
                                       51;
                   Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhatia A;
                                      55; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #10148.
                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Wang SS,
, Jen S, Carter D;
                  8.3%; Score 124.5; DB 20.4%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID No 10447; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                   AAU49252 standard; Protein; 226 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                           295 A----RVLDCYRVLGELE 308
                                                                                                                                                                                                                                                               AAEKKRILHCLGLAEEIQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes
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                             Similarity
315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L'maisonneuve J,
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                                      65;
                                                                                                                                                                                                                                                                                                                                                       AAU49252;
 Sequence
                  Query Match
Best Local :
                                      Matches
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                                                                                                                                                                                                                                                                                                                RESULT 8
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the treatment, prevention and diagnosis of medical conditions caused by paraces. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uvelis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting the sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to chargedulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pct_sequences.
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4
polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde dehydrogenase;
2-pyrone-4,6-dicarboxylic acid; 3,4-dihydroxybenzoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DLPVLPDVDAVIETGIDYCVVAAPTKFHEEIGLKLAEAGVHALIEKPLAYDTAAATRLAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 LAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTSDPLEEDRFGFPAFSGISR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVA- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 MVGIGSMGKNHVRNLR--------AIDGVDLVAIADASGKDPFGVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 122.5; DB 22; Length
23.9%; Pred. No. 0.0012;
Live 21; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hotta Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY68459 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masai E, Fukuda M, Katayama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSLTSALSRTSLATTLTSPR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 LTWLVSLFGELSLVSATLEER 193
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(MAZN ) COSMO OIL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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based on homology with a Zymonoas sp. protein, is believed to be a glucose-fructose oxidoreductase precursor. The DNA sequence was isolated from a library of clones of S. aureus w(UH 29 in Bscherichia coll. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host to may a define a host to graphylococcal infection, e.g. Staphylococcal food polsoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                                                                    The present sequence represents a Staphylococcus aureus protein, that,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVETPSELFKLVDAVVICTPNKFHADLSIEALNHGVHVLCEKPMXMTTEECDRMIEAANK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLKVGVIGVG--GIAQDRHI-----PALLKLKDTVSLVAVQDINTVQMIDVAKRFNIPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 175;
isolate antimicrobial compounds, and in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein fragment SEQ ID NO: 5808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 121.5; DB 27.9%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 KGKVL----HEEHVELLMEEFAFLKKEVVGKDLL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-0127688.
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03-AUG-2000; 2000JP-0280988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                Page 610; 989pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 AA;
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                           aureus infection
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 4
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                                                                                                                                                                                    acid-eta-semialdehyde dehydrogenase (CHMSD) originating in Sphingomonas sp. CR-0310201. CHMSD can be used in the production of 2-pyrone-4,6-dicarboxylic acid by culture of a transformant comprising CHMSD in the presence of a suitable precursor such as 3,4-dihydroxybenzoic acid (which is converted in situ into alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents an alpha-hydroxy-gamma-carboxymuconic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                      New alpha-hydroxy-gamma-carboxymuconic acid eta-semialdehyde dehydrogenase for industrial production of 2-pyrone-4,6-dicarboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IALAGAGAFGEKHLDGLKNIDG----VEIVSIISRKAEQAAEVAAKYGAKHSGTDLSEAL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..175
/note= "residues designated X are not defined in .
    the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of glucose-fructose oxidoreductase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Score 122.5; DB 21;
Pred. No. 0.0016;
3; Mismatches 66;
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Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hodgson JE, I
Rosenberg M,
                                                                                                                 Claim 1; Page 23-25; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 1..175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus
                                                                                                                                                                The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                        280 AA;
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Pratt JM,
                                                                                                                                                                                                                                                                                                                                                             Seguence
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                                                                  acid
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Yokoi H;

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                                                                           The present invention provides a number of nucleotide and protein are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium acids, nucleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
 gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum; carbon metabolism and energy production; SMP Protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; liptid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VVVVGVGRAGSVRMRDLRN------PHPSSAFLNLIGFVSRRELGSIDGVQQIS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum SMP protein sequence SEQ ID NO:288.
                                                SEQ ID NO: 5808; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLL------FTSDP 156
                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 120.5; DB 5.1%; Pred. No. 0.0032;
                                                                                                                                                                                                                                                                                                                                                                                              25; Mismatches
expression profile or pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB79386 standard; Protein; 337 AA
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99DE-1031424.
99DE-1031428.
99DE-1031431.
99DE-1031433.
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99DE-1031413.
99DE-1031419.
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                                                                                                                                                                                                                                                                                                                                                                                                42; Conservative
                                                                                                                                                                                                                                                                                          European Patent Office
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                            337 AA;
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08-JUL-1999;
08-JUL-1999;
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                                                Claim 17;
                                                                                                                                                                                                                                                                                                                            Sequence
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, an incleotide, an inchart compound, a vitamin, a carbohydrate, an arcomatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corranhing them are used for diagnosing the presence or activity of corranhing them are used to map genomes of organisms related to c. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for metabolism of sugars, and in modulating high-energy molecule production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                   Zelder O, Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 120.5; DB 22; Length 337; 25.1%; Pred. No. 0.0032; tive 25; Mismatches 69; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLL------FTSDP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 TVLQVGFNRRFAAGFAAARARIDAGDIGTPQLLRSVTRDPGPFTADP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 550-551; 1246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a cell (1.e. ATP, NADPH).
                                                                                                                                                99DE-1032973.
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                                                              99DE-1032180
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Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061975/07
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                                                                                                                                                                                                                                                                                                                                                                   (BADI ) BASF AG.
                                                                                             09-JUL-1999;
09-JUL-1999;
14-JUL-1999;
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03-SEP-1999;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella comenmoniae, Pseudomonas aeruginosa and Enterococcus facetalis. The preumoniae, Pseudomonas aeruginosa and Enterococcus facetalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to conferring the proteins can be used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery compounds and proteins and evaluates of organisms. The present sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                     Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 346;
                                                                                                             Staphylococcus aureus cellular proliferation protein #1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.9%; Score 119.5; DB 22; 27.9%; Pred. No. 0.0041; ative 21; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW,
                                   AAU36865 standard; Protein; 346 AA.
                                                                                                                                                                                                                                                                                                             2000US-242578P.
2000US-253625P.
2000US-257931P.
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2000US-207727P.
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                                                                                   14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                         Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                   Xu HH;
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                                                                                                                                                                                                 WO200170955-A2
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto RT,
                                                                                                                                                                                                                                                                           21-MAR-2000;
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26-MAY-2000;
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                                                          AAU36865;
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14;
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-----VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                55 VVETPSELFKLVDAVVICTPNKFHADLSIEALNHGVHVLCEKPMAMTTEECDRMIEAANK 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: This patent is in the same patent family as WO200055062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequences isolated from Pyrococcus abyssi encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forterre P, Thierry JC, Prieur D, Dietrich J, 3
Querellou J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.6%; Pred. NO. V...
tive 54; Mismatches 138;
                                                                                                                                 117 KGKVL----HEEHVELLMEEFAFLKKEVVGKDLL 146
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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8 KFCVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67 

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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential cannot the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential cannot have been and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klabbiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The contribiotic development. The antisense nucleic acids can also be used to in proliferation, to express these proteins. To identify proteins used in proliferation, to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an control of the printed specification, but was obtained in electronic form at directly from WIPO at
                                                                                             170 I-----SRLTWL----VSLFGELSLVSATLEERKEDQYMKMTVCLETEKK--SPL 213
                                  174 VIVDLGVHVTDFLRWFFESEPIEVFAVGKAIRGEARVNKTHDHVVMFIKFEGGKTGIGEV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to
                                                                          214 SWIEEKGPGLKRNRYLSFHF----KSGSLE----NVPNVGVNKNIFLKDQNIFVQKLL
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                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #387
                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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Yamamoto RT, Xu HH;
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                                                                                                                                                                                                                                                                              AAU34111 standard; Protein; 341 AA
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26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25738P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                        1 : || : |: 286 STFPQ-AFEAELRHFFECI 303
                                                                                                                                               264 GQFSEKELAAEKKRILHCL 282
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N-PSDB; AAS51970.
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23-MAY-2000;
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68 ------VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGK 119
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                                                                                                                                     11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE--- 67
                                                                                                                                                         23;
                                                                 Length 341;
                                                                 Query Match 7.7%; Score 116.5; DB 22; Length Best Local Similarity 27.8%; Pred. No. 0.0078; Matches 42; Conservative 21; Mismatches 65; Indels
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           120 VL----HEEHVELLMEEFAFLKKEVVGKDLL 146
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Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model.

Run on:

November 1, 2002, 14:43:08 ; Search time 53.7749 Seconds

(without alignments)
952.238 Million cell updates/sec

Title:
US-09-606-129A-3
Perfect score: 1508
Sequence:
1 MNTEPERKFGVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched:
562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 56222
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SPTREMBL_19:*

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1: Sp_archea:*
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3: sp_tungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: Sp_phage:*
10: Sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

			Description	Q96q14 homo sapien	Q9brw8 homo sapien	Q9cy64 mus musculu	Q9dd21 mus musculu	095019 homo sapien	P72782 synechocyst	Q97uh0 sulfolobus	P94437 bacillus su	026961 methanother	Q986t3 rhizobium l	023580 arabidopsis	Q9wz54 thermotoga	Q9vqb3 drosophila	042896 schizosacch	Q9cfc7 lactococcus	Q93ps4 comamonas t
COLUMNICO			ID	Q96QL4	Q9BRW8	Q9CY64	Q9DD21	095019	P72782	097ин0	P94437	026961	0986тз	023580	Q9WZ54	Q9VQB3	042896	Q9CFC7	Q93PS4
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	æ	Query	Match	99.7	9.66	83.9	83.9	30.7	14.4	10.4	9.5	9.4	9.1	9.1	8.8	8.7	8.7	9.8	9.6
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16 Q9BDB4 3 Q13991 17 Q59539 2 O5256 16 Q92ET3 16 Q92ET3 16 Q92X04 2 Q9LXX4 2 Q9LXX4 2 Q9LXX4 16 Q92X8 16 Q92X8 16 Q9CX9 16 Q9CX9 16 Q9CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 2 O5CX9 3 O5CX9 3 O5CX9 3 O5CX9 3 O5CX9 3 O5CX9 4 O5CX9 5 O5CX9 6 O5CX9 6 O5CX9 7 O5CX9 7 O5CX9 7 O5CX9 7 O5CX9 8 O5CX9 8 O5CX9 9 O5CX9 1 O	2 Q9ALN5 11 Q9DBBB 16 Q93ZK4 17 Q9UZ13 16 Q929L3 16 Q929L3 16 Q9WYP5 16 Q9CEL4 2 Q93N64
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MEDLINE-21085660; PUDMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
                                                                                                                                                                                                                                                                                                                                                                         1 MNTEPERKFGVVVVGVGRAGSVRARDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
         241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005902; AAH05502.1; -InterPro; PFR000683; GPO_IDH_MocA. InterPro; PFR000683; GPO_IDH_MocA: 1. PF01408; GPO_IDH_MocA: 1. SEQUENCE 296 AA; 33432 MW; A389AFDDB6ADBABF CRC64;
                                                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                 Score 1502; DB 4;
                                                                                                                                                                                                                                                                                                                          Pred. No. 1.3e-118;
0; Mismatches 1;
                                                                                       296 AA
                                                                                                                                                                                                                         TISSUE-BRAIN, PRIMITIVE NEUROECTODERMAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                            Created)
                                                                                                                                           SIMILAR TO BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                               99.68;
                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 2500001N03RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.7
Matches 295; Conservative
                                                                                       PRELIMINARY;
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                                                                                                           01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2500001N03RIK.
                                                                                                                                                                                                                                                                                                                 Query Match
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Q9CY64;
                                                                                               Q9BRW8;
                                                                                     Q9BRW8
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                                                                RESULT 2
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Astons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Boris A., Yoshida K., Wang K.H., Weltz C., Whittaker C., Wilming L., Angashizaki Y., Stork K.H., Weltz C., Whittaker C., Wilming L., Rashibati Y., Stork K.H., Weltz C., Whittaker C., Wilming L., Rashibati Y., Stork K.H., Weltz C., Whittaker C., Wilming L., R., Phinchtick C., Whittaki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 DALRSQEVDVAYICTESSSHEDYIRQFLQAGKHVLVEYPMALSFAAAQELWELAAQKGRV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; mature 4090;685-690(2001).
EMBL; AR010847; BAB2713.1; -.
MGD; MGI:1917355; 2500001N03Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.9%; Score 1264.5; DB 11; Length 295; 83.9%; Pred. No. 1.4e-98; ive 26; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 VPNVGVNKNIFLKDQDIFIQKLLGQVSAEDLAAEKKRILHCLELASDIQRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F2E1682BD77032A4 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=KIDNEY;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000683; GFO_IDH_MocA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01408; GFO_IDH_MocA; 1
SEQUENCE 295 AA; 33524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 83.9 ses 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
0610006AllRIK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 HIELLGGVHQAIRQNLGKIGEVFYARYSTIMGQNPAPQRWTYHHQQFGFPLVAALSRISR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 LVSLFGELSLVSATLE--ERKEDQYMK---MTVCLETEKKSPLSWIEEKGPGLKRN-RYL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 FTDLFGTVQQVDAQCRFWDQPNPEYFRACLATAYLQFNNGLKAEVIYGKGEVFHQNERIF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 SFHFKSGSL------ENVPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQEVEVAY ICSESSSHEDY IRQFLNAGKHVLVEY PMTLSLAAAQELWELAEQKGKVLHEE 124
                                           1 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSID-----GVQ-QISLEDALS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 VGIVGTGYAAQRRAEVFRGDRRS----QLVSFWGNSEANTAKFADTFGVRPQQSWQALIN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S. Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 AA; 36640 MW; 51474ABD26B2C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 217; DB 16; 24.9%; Pred. No. 3.2e-10; iive 57; Mismatches 139;
                                                                                                                                                                                                                   AA.
                                                                                                              LFGELSLVSATLEERKEDQYMKMTVCLETEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90900; BAA16797.1; -
InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01408; GFO_IDH_MOCA; 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
Complete proteome.
SEQUENCE 328 AA; 36640 MW; 51.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.9%;
Matches 79; Conservative
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                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                BILIVERDIN REDUCTASE.
SLR1784.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1148;
                                                                                                                                                                                                                                   P72782;
                                                                                                                                                                                                                 P72782
                                                                                            179
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                                                                                                                                                                             RESULT 6
P72782
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Q97UH0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
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                                                                                                                                                                                                                                                                                                                                                                                                         1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE 60
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.E., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasakl H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Manng K.H., Wetzz C., Whittaker C., Wilming I. Wynshaw-Boria A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                  DB 11; Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 VPNVGVNKNIFLKDQDIFIQKLLGQVSAEDLAAEKKRILHCLELASDIQRLC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 463; DB 4; Length 92
Pred. No. 9.7e-32;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cordes M., Wohldman P., Morris M.;
"The sequence of Homo sapiens PAC clone RP5-974M14.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                34491 MW; 52D8A3B02EE956EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AA; 10552 MW; 390331108449BD93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                  83.9%; Score 1264.5; DB
83.9%; Pred. No. 1.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AA.
                                                                                                                                                                                                                                                                                                                                                   26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BILIVERDIN-IX ALPHA REDUCTASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                        Nature 409:685-690(2001).
EMBL; AK002231: BAB21950.1; -
MGD; MGI:1915580; O610006A11Ri.
InterPro; IPR000683; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA; 1.
SEQUENCE 303 AA; 34491 MW; 52Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1999) to the EMBL; AC004939; AAD05025.1;
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.9
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Conservative
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                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
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Matches 92
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11;

42; Gaps

Length 328; Indels

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RAK WIDLINES-9144403; PubMed-31843/;
RAK KUNST E., Oggaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broizof F. V., Deviner K.M., Dusterhoft A., Erliich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Febret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Melain C.,
RA Kurita K., Lapidus A., Lardinois S., Hauber J., Lazarevic V.,
A Codyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Brato V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Reger M., Rivolta C., Roche B., Rose M., Sadaie Y.,
Schleich J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Schleich J., Schleich S., Schroeter R., Yognantu K.,
RA Tosato V., Uchlyama S., Vandenbol M., Vannen K., Yasumoto K., Yata K.,
Whiters P., Wipat A., Yamannoto H., Yamane K., Yasumoto K., Yata K.,
Whiters P., Wipat A., Yamannoto H., Yamane K., Yasumoto K., Yata K.,
Whiters P., Wipat A., Yamannoto H., Yannen E., Woolterlum Bacillus
RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
Ray Voshikawa H.F., Zumstein E., Woolterlum Bacillus
RA Purra Such A.
                                                                                         Yamamoto H., Uchiyama S., Sekiguchi J.; "The Bacillus subtilis chromosome region near 78 degrees contains the genes encoding a new two-component system, three ABC transporters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQKGKVLHEEH----VELLMEEFAFLKKEVVGKDLLKGSLLFTAG---PLEEERFGF--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 QQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; 209108 CAB11399.1; ... EMBL; 299108 CAB12657.1; ... InterPro: IPR000683; GFO_IDH_MOCA. InterPro: IPR004104; GFO_IDH_MOCA_C. Pfam; PF01894; GFO_IDH_MOCA_C. Pfam; PF01894; GFO_IDH_MOCA_C. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA; 43584 MW; 3EEE326E1A047602 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VVGVGRAGSV----RMRDLRNPHPSSAF-LNLIGFVSRRELGSIDGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%; Score 143; DB 16; ilarity 24.4%; Pred. No. 0.0007; Conservative 52; Mismatches 97;
                                                                                                                                                                                                                                                                                       MEDLINE=98044033; PubMed=9384377;
                                                                   MEDLINE=97128783; PubMed=8973323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).
                                                                                                                                                                                        Gene 181:147-151(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :99
                                                                                                                                                                                                                                                                   STRAIN=168;
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 35092 / DSM 1617 / P2;

X MEDLINE-2132295; bubMed-11427726;

X MEDLINE-2132295; bubMed-11427726;

X Awayez M.J. Chan-Weilher C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J. Chan-Weilher C.C.-Y., Clausen I.G., Curtis B.A.,

A wayez M.J. Chan-Weilher C.C.-Y., Clausen I.G., Curtis B.A.,

A moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffichs A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A Garrett R.A., Ragan M.A., Sansen C.W., Van der Oost J.;

A Garrett R.A., Ragan M.A., Sansen C.W., Van der Oost J.;

RT The complete genome of the crearchaeon Sulfolobus Solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

B FRBL, ABC06896; AR43149; FPOLDH_MOCA.

RITERPRO; IPR004104; GFO_IDH_MOCA.

R Ffam; PF01408; GFO_IDH_MOCA.

PR Ffam; PP02894; GFO_IDH_MOCA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRIGVAVVGLGSIGKTHVKALKDLEKETEFVKLVAVVDQIKAIAEKIGSEYGTPYYTTID 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VEDTAVAIMR-----YKNGALGTISQTVSMKPTTYQYRKIRVNGSNGFVEITDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 RKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGEVSR-----RELGSIDGV-QQISLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 WRGMWNTEGGGVMTNQGIHTIDLMIWLNGEVEEVSGFVDNLTHDG-----IE-----
                                                                                                                                                                                           Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 AA; 41760 MW; DAAE16466D53306B CRC64;
                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 157.5; DB 7 Pred. No. 3.9e-05;
371 AA
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NCBI_TaxID=1423;
                                               Created)
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : | : | : | : LSTVAIEGKIEESKSSVEYKK 307
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PRELIMINARY;
                                          01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                  DEHYDROGENASE, PUTATIVE
                                                                                                                                                                  Sulfolobus solfataricus
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Best Local Similarity
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A MEDLINE-98037514;

A MITTED BROOTSTEEL STRAME L.A., DeLoughery C., Lee H.-M., DuBois J.,

A MITTED B. Bashitzadeh R., Blakely D., Cook R., Gilbert K.,

A MITTEON D., Hoang L., Kaglae P., Lumm W., Pothier B., Qiu D.,

A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

A Juwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

A Daniels C.J., Mao J.-I., Rice P., Nolling J., Reve J.N.;

T. Complete genome sequence of Methanobacterium thermoautotrophicum

R. Complete genome sequence of Methanobacterium thermoautotrophicum

R. Daniels C.J., Mao J.-I., Rice P., Nolling J., Reve J.N.;

T. Bacteriol. 1797135-7155(1997).

B. BREL, AE000863; ARB85373.1;

B. BREL, AE000863; GFO_LIDH_MocA.

InterPro: IPR004104; GFO_LIDH_MocA.

InterPro: IPR004104; GFO_LIDH_MocA.

BREN PF040894; GFO_LIDH_MocA.C:

BREN PF040894; GFO_LIDH_MocA.C:

BON Pfam: PF020894; GFO_L
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121 GHVERFNPAVQKAKELIENDVIGDVVSASAKRVGPFPPRIKDVGVTIDLAIHDLDVMHYL 180
             ----PAFSGISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPL----SWI 216
                                      193 WRVDPAIAGPS-----FVLGDLS-----THTYYMSQLIMPKMKIKELLCDRQSFV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DuBois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FSEPVAEVYAVMGSILEKCEYEDHAEIMTKFKSG------ITGILEVNWLTPYKR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RKFGVVVVGVGRAGSVRMR---DLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDAL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RQINVGVIGVGAMGYNHARVYYRLKNAN-LMAVSDIMKGTLOKVANKYDTVGYVDYENLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LKGSLL-----FTACPLEERFGFPAFSGISRLTWL----
                                                                                                                                                                                                                                                                                                                                    Methanothermobacter thermautotrophicus.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-CHLOROBENZOATE-3,4-DIOXYGENASE DYHYDROGENASE RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 141; DB 17
Pred. No. 0.00077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKLAITGTDGIINVDYIDQRLDVYGKFAQDVDIKHEEPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Mismatches
                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382
                                                                                     EEKGPGLKRNRYLSFHFKSGSLENVPNVGVN 247
                                                                                                                        GSRAP-LEDNAHVLMHYENGAVGTMWTSSIN 267
                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 EHVE----LLMEEFAFLKKEVVG---
                                                                                                                                                                                                                                                                    (TrEMBLrel. 05, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DELTA H;
                                                                                                                                                                                                                                                                      01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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Q986T3
ID Q986T3
                                                                                                                                                                                                                   026961
             165
                                                                                                                        238
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                                                                                                                                                                              RESULT 9
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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Romplete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWELABOKGKVLHE------EHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ERF---GFPAFS-GISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSW 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSID----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 FYYOPGGPVFDMGPYYLTMLVNLLGPVARVMAMATRGOEERL-------
                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacterial: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBL_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
10-DEC-2001 (TrEMBLR-E). 19, Last annotation update)
INOSITOL 2-DEHYDROGENASE HOMOLOG (INOSITOL 2-DEHYDROGENASE LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90121113: PubMed-9461215;
Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Kato T., Sass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.1%; Score 137.5; DB 16; Length 382; 23.7%; Pred. No. 0.002; Live 39; Mismatches 105; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40593 MW; 785DA27E3D3308C5 CRC64;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|| :|| | : || |: || | ITAEGP-----FKNTTFKVGTPTNV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEEKGPGLKRNRYLSFHFKSGSLENV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AP003011; BAB53370.1, -.
InterPro. IPR000683; GFO_IDH_MocA.
Pfam. PF01408; GFO_IDH_MocA; 1.
COMPLETE proteome.
SEQUENCE 382 AA; 40593 MW; 7851
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 23.7% 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-MAFF303099;
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                                                                                                      DEHYDROGENASE
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12;

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Query Match
Best Local Similarity
                                                                                                                                                 Complete proteome. SEQUENCE 360 AA;
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CG3597 PROTEIN.
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Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H., Wedler E., Wambutt R., Weizenegger T., Pohl T.M., Terryn N., A Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A., Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P., Entian K.D., Rigger M., Schaeffer M., Funk B., Mueller-Auer S., A Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A., A Woukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C., Pelseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S., Schueller C., Chalwatzis N.; Maves H.W., Klosterman S., Tanalysis of 1.9 Mb of contiguous sequence from chromosome 4 of Nature 391:485-488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GISRL-TW------LVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGK--HVLVEYPMTLSLAAAQE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------PVCVMASGGMDVNHK 220
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         KFGVVVVG-VGRAGSVRMRDLR-----NPHPSSAFLNL----IGFVSRRELGSI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 KYGIVGIGMMGREHLINLHHLRDQGLAVVCIADPHPPSQLLAIELAQSFGW----ELKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 LWELAEQKGKVLHEEHVEL-LMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VLEAAKKRSDMVVQVGLEYRYMPPVAKLIEQVKGRDF--GNVKMVA--IREHRFPFLVKV
                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297343; CAB10518.1; -.
                                                                                                                                                                                                                                                                 EMBL; AL16184; CAB10518.1; -.
EMBL; AL161846; CAB78740.1; -.
InterPro; IPR000683; GPO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA_C.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
SEQUENCE 364 AA; 40260 MW; B56312BD6CF01B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN BPLA.
                                                                                                                                                                                                                                                                                                                                                                               9.1%; Score 136.5; DB 10;
23.1%; Pred. No. 0.0022;
tive 49; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 AA.
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Bacteria; Thermotogales; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 EE----KGPGLKRNRYLSFHFKSG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 DEVYGGKVPDIIDNAYVIIEFDNG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel, 12, 01-NOV-1999 (TrEMBLrel, 12, 01-DEC-2001 (TrEMBLrel, 19,
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                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Ashton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.W., Basch A., Baxendale J., Bayraktaroglu L., Beasaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Blotlakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
Acherry J.M., Cawley S., Dahlke C., Busen R., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Felrischmann W.,
Abrosher C., Gabrielian A.E., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
EMBL; AE001733; AAD35670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 KQKN-----QNRFNPPVQEVRKKLD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SGAFGKIFYASVAWNRNEDYYKOA-----SWRGTWEMDGGVLMNO--STH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 --ISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 EQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLRIALVGCGRIGQKKHVPALIETQDL---FETVAVCDLVEERANRAAEHFEKSGLRRPE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 KFGVVVVGVGRAGS-----VRMRDLRNPHPSSAFLNLIGFVSRRELGSID--GVQQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; Score 132; DB 16; Length 36
%; Pred. No. 0.0053;
37; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           3B17BCD4A94A6EC6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 -----FKSGSLENVPNVGVNKN---IFLKDQNIFVQKLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 AIDLLQWFLGGEIEEIYGHIANTNHPYIEAEDEGFAIVKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
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                                                                                                                                                                                       Interpro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
InterPro; IPR0034189; Ribosomal_S30.
Pfam; PF01408; GFO_IDH_MOCA; I.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA; 41023 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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us-09-606-129a-3.rspt

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SEQUENCE FROM N.A.
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

A Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Glibs R.A., Myers E.W., Kubin G.M., Venter J.C.;

RH Glibs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RH Glibs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RH The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

RHUSH, AEOROSS83; AAFS1283.1;

BRINBL, AEOROSS83; AAFS1283.1;

BRINBL, REOROSS83; AAFS1283.1;

BRINBL, REOROSS83; AAFS1283.1;

BRINBL, REOROSS83; ARCOLDH_MOCA.

InterPro; IPR0040683; GFO_LDH_MOCA.C.;

RT Pfam; PF01408; GFO_LDH_MOCA.C.;

REMB. PF01408; GFO_LDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNTEPERKFGVVVVG-----VGRAGSVRMRDLRNPHPSSAFLNLIG-----FVSRREL- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE C115.03 IN CHROMOSOME II (EC 1.-.-).
SPBC115.03 OR SPBC24E9.18C.
SPBC115.03 OR SPBC24E9.18C.
SCHIZOSACHAROMYCES pombe (Fission yeast).
Eukaryota; Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 130.5; DB 5; Length 335; 23.2%; Pred. No. 0.0064; tive 43; Mismatches 96; Indels 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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279 F-DFHY 283
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10 04289
AC 04289
DT 01-JU
DT 01-JU
DT 01-DE
DE HYPOT
GN SPBC1
GN SPBC1
GN SPBC1
CO SChiz
OC SChiz
OX NCBIL
RN [1]
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"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sp. lactis LL1403.";

EMBL, AE006386; AAK05652.1;

InterPro; IPR000683; GFO_IDH_MocA.

Pfam; PF01408; GFO_IDH_MocA.

SEQUENCE 324 AA; 36603 MW; DBF47D6684EB259C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 VLVEYPMTLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 SAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKH 93
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

-: SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES.
EMBL, ALO22105; CAA17915.1; -.
INTERPRO; IPR000683; GFO_IDH_MOCA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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MEDLINE-21235186; Pubmed-11337471;
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SEQUENCE 368 AA; 41271 MW;
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Job time: 55.7749 secs

us-09-606-129a-3.rsp

7

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:41:32; Search time 15.2283 Seconds (without alignments) 752.611 Million cell updates/sec Run on:

US-09-606-129A-3 1508 1 MNTEPERKFGVVVVGVGRAG......RILHCLGLABEIQKYCCSRK 296 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	BIEA HIMAN	BIEA RAT	YHHX_ECOLI	Y816_SYNY3	YVAA_BACSU	YULF_BACSU	YRBE_BACSU	YM94_YEAST	YMO1_RHIME	CBAC_COMTE	GFO_ZYMMO	MVIM_ECOLI	YDGJ_ECOLI	PHT4_PSEPU	ANFA_AZOVI	RPOB_ASTLO	YISS_BACSU	RPOC_MYCTU	G160_HUMAN	SPCA_HUMAN	TNP6_ENTFC	GOG4_HUMAN	YGJR_ECOLI	SMCY_MOUSE	YH58_AQUAE	.DING_BACSU	MVIM_SALTY	FLIF_BUCAI	FAS1_YEAST	MI2D_RHIME	MYH9_CHICK	VATI_METJA	HMMR_HUMAN
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AK1H_SERMA	TIG_BORBU PHYB_SOYBN	G160_MOUSE YIO9_YEAST	YJHC_ECOLI SCP1_MOUSE	TANA_XENLA UGA3_YEAST	PRE_STRAG PYRB_PYRHO
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# ALIGNMENTS

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BIEA	NESOLI I BIEA HUMAN
OI.	BIEA_HUMAN STANDARD; PRT; 296 AA.
A E	
2 5	01-OCT-1996 (Rel. 34, Last sequence update)
DŢ	(Rel. 40, Last annotation update)
DE	ч
DE	reductase)
Z C	BLVRA OR BLVR OR BVR.
3 5	AUNIO Sapletis (Mundal) Bukarvota - Matazoza Chordata Craniata Vertebrata Buteleosfoni
3 6	
38	NCBI TaxID=9606:
RN	[1]
RP	SEQUENCE FROM N.A.
ည္	TISSUE-Placenta;
ž :	,
A E	Maines M.D., Polevoda B.V., Huang TJ., McCoubrey W.K. Jr.;
RT	numen biliverulm inaipme reductase is a zincimetallopioteim. Characterization of purified and Escherichia coli expressed
R	CONTROL OF PRINCIPLE OF PRINCIPLE CONTROL OF
R.	J.
RN	
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RA	Komuro A., Tobe T., Nakano Y., Yamaguchi T., Tomita M.;
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ж. С.	SEQUENCE OF 1-11/ FROM N.A.
\$ 5	COLOGS M. WOLLTAN C., Callel I.; Colomitted TIME-1000, to the Buns (Control Astrobook
7 2	tabilitied (JON-1996) to the EmbLycenbank/DDBJ databases.
Z 0	14 1 SPOTIENCE 3-36. 49-74 AND 228-248
יי ל ב	DECORPORATION OF U.S. ACCUSANCE AND STREET S
X X	MEDLINE-93143333; Pubmed-8424666;
RA	Maines M.D., Trakshel G.M.;
RT	"Purification and characterization of human biliverdin reductase.";
RL	Arch. Biochem. Biophys. 300:320-326(1993).
RN	[5]
RP	SEQUENCE OF 3-22.
S S	TISSUE-LIVER:
XX	MEDLINE=95014177; PubMed=7929092;
A E	Yamaguchi T., Komoda T., Nakajima H.; "Dilinordin-IV slobs roductson and hijinordin-IV bots roductson from
R. E.	billycidin in alpha feduciase and billycidin in beca feduciase from human liver. Purification and characterization.":
R.	J. Biol. Chem. 269:24343-24348(1994).
<u>ဗ</u>	-! - FUNCTION: CONVERTS BILIVERDIN TO BILIRUBIN.
ပ္ပ	-!- CATALYTIC ACTIVITY: Bilirubin + NAD(P)(+) = biliverdin + NAD(P)H.
႘	
ပ္ပ	SPECIFICITY. USES NADH AT THE ACIDIC PH RANGE (6-6.7) AND NADPH AT
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ဗ္ဗ	-!- PATHWAY: FINAL STEP IN HEME METABOLISM.
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ည	-!- SIMILARITY: TO E.COLI YHHX.

Evidence suggesting the liver and kidney enzymes are the

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reductase.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fakhrai H., Maines M.D.; "Expression and characterization of a cDNA for rat kidney biliverdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
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D -> E (IN REF. 2).
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                                                                                                                                              Interpro; IPR000683; GFO_IDH_MocA. Pfam; PF01408; GFO_IDH_MocA; 1. Oxidoreductase; NAD; NADP; Zinc.
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MEDLINE-92156147; Pubmed-1371282;
                                                                                                EMBL; X93086; CAAG3635.1; -.
EMBL; U34877; AAC35588.1; -.
EMBL; AC005189; AAC25526.1; -.
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                                                                                                                 MCCOUNTEY W.K. Jr., Maines M.D.;

T "Site-directed mutagenesis of cysteine residues in biliverdin mitagenesis of cysteine residues in biliverdin mutagenesis of cysteine residues in biliverdin reductase. Roles in substrate and cofactor binding.";

Eur. J. Blochem. 22:597-603(1994).

-!- FUNCTION: CONVERTS BILIVERDIN TO BILIRUBINS. DISPLAYS TWO DISTINCT PH OPTIMA USING A DIFFERENT COPACTOR PH: NADH AT THE LOWER PH OFTIMA USING AND NADHA AT PH 81.5-8.7. NADPH, HOWEVER, IS THE PROBABLE COFACTOR IN BIOLOGICAL SYSTEMS.

-!- CATALYTIC ACTIVITY: Bilirubin + NAD(P)(+) = biliverdin + NAD(P)H.

-!- COFACTOR: BINDS ONE ZINC ION.

-!- PATHMAX: FINAL STEP IN HEME METABOLISM.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SUBCELLULAR LOCATION: Cytoplasmic.
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C->A: REDUCED ACTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1247.5; DB Pred. No. 1.2e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M81681; AAA40830.1; -.
InterPro; IPR000683; GFO_IDH_MOCA.
Pfam: PF01408; GFO_IDH_MOCA.
Oxidoreductase: NAD: NADP: Zinc.
                     Biol. Chem. 267:4023-4029(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC
ZINC
ZINC
ZINC
                                                                                               MEDLINE=94291657; PubMed=8020496;
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transcript product.
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16
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295 AA;
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                                                                          MUTAGENESIS
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STRAIN-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 V 158
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVAA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAG-----PLEEERFGFP---AF-- 167
                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                      11- SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 345;
                                                                                                                                                                                                                                                                        MEDLINE-99420866; PubMed-10493123;
Fountculakis M., Takacs M.F., Berndt P., Langen H., Takacs E
"Enrichment of low abundance proteins of Escherichia coli by
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Complete proteome.
SEQUENCE 345 AA; 38765 MW; 31D73A62511C7F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase sll0816 (EC 1.-.-.).
SLU0816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 151.5; DB 1
31.3%; Pred. No. 0.00012;
tive 27; Mismatches 52
       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative oxidoreductase yhbx (EC 1 - - -)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 AA.
                                                                                                                                                                                                                                                             IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECGEDE, EG12944; yhhx.
InterPro: IPR000683; GFO_IDH_MOCA.
InterPro: IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA_C.
Pfam; PF02894; GFO_IDH_MOCA_C: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U18997; AAA58238.1; -.
EMBL; AECO0420; AAC76465.1; -.
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVHTMDQIISLFG 188
                                                                       Escherichia coli
                                                                                                          NCBI_TaxID=562;
                                                           YHHX OR B3440
                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y816_SYNY3
P74041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 -- EVQVIPDFEFRFVPAWQYVAELLGQGIL------GQLK-----LIKVDWL 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VAVIGTGFGQAVHIPALQYHQQTQAIA----IYHRDLAKAQEVAKSNDLAYSYNNLEEL 63
                                                                                                                                                                                                                                      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YHHX FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000683; GFO_IDH_MocA.
InterPro: IPR004104; GFO_IDH_MocA_C.
Pfam: PF01408; GFO_IDH_MocA_C.
Pfam: PF02894; GFO_IDH_MocA_C.
Pfam: PF02894; GFO_IDH_MocA_C.
Alpothetical protein; Oxidoreductase; Complete proteome SEQUENCE 371 AA; 41489 MW; BDEFE020D4D84BF6 CRC64;
Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase in FHUD-OPUBD intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:109-136(1996).
-!- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 130.5; DB 1;
26.0%; Pred. No. 0.0056;
ative 33; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                     MEDLINE-97061201; Pubmed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90911; BAA18116.1; -.
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Matches 47; Conservative
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                                                                                                                                                                 SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                    148 GSL-----
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005389;
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                                                                                                                                                     SEQUENCE
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                 DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                           EITNDPAIELVIVTTPSGLHYEHTMACIQAGKHVVMEKPMTATAEEGETLKRAADEKGVL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 LSVYHNRRWDNDFLTIKK-----LISEGSLEDINTYQVSYNRYRPEVQARWRE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 ILY--------GGSI--VPANGPRYQIHGKDSSFIKYGIDGQ--EDALR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO E.COLI
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                                                                                                                                                                                                                                                                                                                             RKFGVVVVGV---GRAGSV---RMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFGFPAFS----GISRLTWLVSLFGELSLVSATLEERKED----QYMKMTVCLETEKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 LSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVNKNIFLKDQNIFVQKLLGQFSEKELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouder B., Koningsteyn G., Feger G., Pohl T.; Ouder Beatilus genome sequence project: sequence of mcp/tlp to yulf; a segment of the Bacilius genome at about 276 degrees."; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases:
-1- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY. STRONG, TO E.C
                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                     Length 358;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                         sctase; Complete proteome. 532C4DB37CEB1570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEE-----
                                                                                                                                                                                                                                                  8.1%; Score 122.5; DB 1;
21.7%; Pred. No. 0.022;
ve 49; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
14. Mark-2002 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase yulf (EC 1. . . . . )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis,
Bacteria; Firmicutes; Bacillus/Clostridi
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                         n; Oxidoreductase;
40112 MW; 532C4DE
                                                                                                                                      SubtiList; BG14057; yvaA.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
                                                                                                                                                                            Pfam; PF01408; GFO_IDH_MOCA; 1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
Hypothetical protein; Oxidoreducts
SEQUENCE 358 AA; 40112 MW; 53.
                                                                                                                        EMBL; 299121; CAB15358.1; -.
                                                                                                                                                                                                                                                                Best Local Similarity 21.79
Matches 66; Conservative
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                                                                                                                                      SubtiList; BG14057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AGRK 273
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15-DEC-1998 (
01-MAR-2002 (
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=9717783; PubMed=9025289;
Gomez M., Cutting S.M.;
Boff encodes a putative forespore regulator of the Bacillus subtilis sigma K checkpoint.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KDLLK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LFTAGPLEEERFGFPAFSGISR----LTW----LVSLFGELSL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 VSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 LQEMAASDCFDAVYIASPNALHKEQAVLFMNHGKHVLCEKPFASNTKETEEMISAAKANG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 VVLMEAMKTTFLPNFKELKKHLHKIGTVRRFTASYCQYSSRYDAFRSGTVLNAFQPELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tosato V., Bolotin A., Bertani I., Valentino I., Bruschi C.V "A 17 8 kb segment in the spov9-add region of the Bacillus 1168 chromosome: sequencing and ruv operon identification."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 VNKNIFLKDQNIFVQKLLGQFSEKELAAEK - - - KRILHCLGLAEEIQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 PKPAMFYE----AEEFVTLIKENKLESEENTFERSLTTAKIMEEARK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                 EMBL; 29919; CAB07947.1; -.
EMBL; 299119; CAB15095.1; -.
Subtilist; BG12388; Yulf.
Interpro; IFR001068; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA. 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                             53134AD13A4B2835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 143:157-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101;
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase yrbE (EC 1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 KVLHEEHVELLMEEFAFLKKEV--VG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 119.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus group; Bacillus
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30-MAY-2000 (Rel. 39, Last seq
16-OCT-2001 (Rel. 40, Last anno
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Pred. No.

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Best Local Similarity
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entities requires a.license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            66 DIDAIFICSPTAVHAQMIKEAAEAKKHIFCEKPVSFSLDETSEALAAVRKHGVTLQVGFN 125
                                                                                                                                                                                                                                                                                                                                                122 ----HEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEBRFGFPAFSGISRLTWL 176
                                                                                                                                                                                                                                                                                                                                                                  126 RRFDPHFKKIKTIVE-----NGEIGTPHLLK----ITSRDPEPPNIDYVRTSG----- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C / AB972;
Churcher C.M., Louls E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (NOY-1995) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: SOME, TO THE YHHX FAMILY OF OXIDOREDGCPASES.
                                                                                                                                                                                                                                                                                             EVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVL---- 121
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                       13 VVGVGRAGSVRMRDL-RNPHPSSAFLNLIGFVSRRELGSIDGVQQI-----SLEDALSSQ 66
                                                                                                                                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 38.2 kDa protein in PRES-FET4 intergenic region.
                                                                                                                                                                                     Length 341;
                                                                                                                                             al protein; Oxidoreductase; Complete proteome. 341 AA; 37788 MW; E3023CD874F90C5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77C7F72321BCAD1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                  7.2%; Score 108; DB 1;
21.7%; Pred. No. 0.28;
tive 33; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 AA
                                                 EMBL; 299118; CAB14737.1; --
EMBL; 293081; CAA63619.1; --
SUBLILISE; BGI2280; yrbE.
InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR001104; GFO_IDH_MOCA.
FRAM; PF01408; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD: SOO04932; YMR315W.
InterPro: IPRO00683; GFO_IDH_MocA.
InterPro: IPRO04104; GFO_IDH_MocA.C.
Pfam; PFO1408; GFO_IDH_MocA.C.
Pfam; PFO2894; GFO_IDH_MocA.C.
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                                     EMBL; Y15896; CAB75327.1; -.
                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
349 AA; 3
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                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     177 VSLFGELSL 185
                                                                                                                                                                                                                                                                                                                                                                                                                              170 -GLFMDMSI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                             Hypothetical
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SEQUENCE 34
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Q04869;
                                                                                                                                                           SEQUENCE
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Matches
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DB 1; Length 349;

7.0%; Score 105.5;

Query Match

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01-FEB-1996 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 36.4 kDa protein in mocC-mocA intergenic region (ORF334).
Rhizoblum melliOti (Sinorhizobium mellioti).
Bacteria: Proteobacteria: alpha subdivision; Rhizoblaceae group;
Rhizoblaceae; Sinorhizoblum alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 GK------VLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERF- 162
                                                                                                                                                                                                                                                                                                                                                                                           77 HEHVHWAIRAAEAGKHVLCEKPLALDVEELSRLIDCRDRTGRRIQEAVMIRAHPQWDEIF 136
                                                                                               SLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK 117
                                                                                                                                    60 NLDEILNDPHVDXIDALLPAQFNADIVEKAVKAGKPVILEKPIAANLDQAKEIVKIAEST 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 SSAFLNLIGEVSR-------RELGSIDGVQQISLEDALSSQEVEVAYICSES 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95147842; PubMed-7845353; Rossbach S., Kulpa D.A., Rossbach U., de Bruijn F.J.; Rossbach S. Kulpa D.A., Rossbach U., de Bruijn F.J.; "Molecular and genetic characterization of the rhizopine catabolism (mochBRC) genes of Rhizobium mellicti L5-30."; Mol. Gen. Genet. 245:11-24(1994).
-:- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
                                                                                                                                                                                                                                                                                                                                                       163 GFPAFSGISRLTWLVSLFGELSLVSATLEERKE----DQYMKMTVCLETEKKSPLSWIEE
                                                                                                                                                                                                                                                                                        PLPVGVAENWLYLPCIKIAKEQIEKIGPVVAFTHNS-TGPFVTQNKYLTTTWRQKPEHIG
                                    43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                             87; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 SSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE--
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-----KNKEVIGSFTYGSAFG----ATEKSVFLK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 KGPGLKRNRYLSFHFKSGSLENVPNVGVNKNIFLK 253
   0.45;
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                                    Mismatches
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InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA; I.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
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                                 38;
21.9%;
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=382;
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                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMO1_RHIME
P49305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                             Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VVGVGRA------GSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLED 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VVGLGKAFMLMLPTFLMDRRVQLVAASDTDP----LSLRQFKADFPAAAVHG----DIES 56
                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1-carboxy-3-chloro-3,4-dihydroxycyclo hexa-1,5-diene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucose--fructose oxidoreductase precursor (EC 1.1.99.28) (GFOR).
                                                                                                                                                                                                                                                                                             for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 397;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BR60 / ISOLATE BLOODY RUN CREEK; TRANSPOSON=Tn5271;
MEDLINE=97464069; PubMed=9322760;
MEDLINE-97464069; Providenti M., Wyndham R.C.;
The cis-diol dehydrogenase cbaC gene of Tn5271 is required growth on 3-chlorobenzoate but not 3,4-dichlorobenzoate.";
Gene 196:209-218[1997]...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Aromatic hydrocarbons catabolism.
SEQUENCE 397 AA; 44090 MW; EAD6115ECD61C042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
           165 ------PAFSGISRLTWLVSLF---GELSLVSAT 189
                        197 VFAVSDLDPVF-GIDRLTSAVLLFPGGRQATLVVST 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103.5; Di
Pred. No. 0.76;
                                                                                               397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam: PF02894; GFO_IDH_MOCA_C.
Pfam: PF02894; GFO_IDH_MOCA_C: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18133; AAC45718.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zymomonas mobilis.
                                                                                                                                                                                                                     NCBI_TaxID=285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IVGH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 HEEH 125
                                                                                              CBAC_COMTE
044258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFO_ZYMMO
Q07982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: D-glucose + D-fructose = D-gluconolactone + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucitol.
-!- COFACTOR: CONTAINS ONE TIGHTLY-BOUND NADP(H) MOLECULE PER SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRSFKAGKHVMCEKPMAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:|| :||:||:||
81 DRRFGYAIVGLGKYA-------LNQILPGFAGCQHSRMKLWSAVTEKAKIV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DGVQQISLED-----ALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTL 102
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-71 FROM N.A., AND SEQUENCE OF 2-16 AND 53-71.
STRAIN=ATCC 29191 / ZM6, AND ATCC 31821 / ZM4 / CP4;
MEDLINE=93231476; PubMed=8472911;
LOOS H., Sahm H., Sprenger G.A.;
"Glucose-fructose exidoreductase, a periplasmic enzyme of zymomonas mobilis, is active in its precursor form.";
FEMS Microbiol. Lett. 107:293-298(1993).
                                                                                                                                                                           Kanagasundaram V., Scopes R.K.;
Lioning, sequence analysis, and expression of the structural gene
encoding glucose-fructose oxidoreductase from Zymomonas mobilis.";
J. Bacteriol. 174:1439-1447(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97148336; PubMed-8994968;
Kingston R.L., Scopes R.K., Baker E.N.;
"The structure of glucose-fructose oxidoreductase from Zymomonas
mobilis: an osmoprotective periplasmic enzyme containing non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNL1 - GFV - - - SRRELGSI - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCOSE--FRUCTOSE OXIDOREDUCTASE.
L -> Q (IN REF. 2; AA SEQUENCE).
C1E4A19F5B34267A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels
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Pfam; PF02894; GFO_IDH_MocA_C; 1.
Oxidoreductase; NADP; Signal; Periplasmic; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- PATHWAY: SORBITOL-GLUCONATE PATHWAY.
-I- SUBUNIT: HOMOTETRAMER.
-I- SUBCLLULAR LOCATION: PETIPLASMIC.
-I- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.7%; Score 101.5;
                                                                     AND SEQUENCE OF 53-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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EMBL; X73088; CAA51534.1; --
PDB; 1.OFG; 21-APR-97.
InterPro; IPR000683; GFO_IDH_MocA.
InterPro; IPR004104; GFO_IDH_MocA_C.
                                                                 SEQUENCE FROM N.A., AND SEQUENCE C
STRAIN-ATCC 29191 / ZM6;
MEDLINE-92165717; PubMed-1537789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 439 G
61 61 L
439 AA; 47801 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dissociable NADP.";
Structure 4:1413-1428(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 SLAAAQELWELAEQKGKVL 121
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nes 36; Conservative
NCBI_TaxID=542;
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Hypothetical
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Q05184;
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PHT4_PSEPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                        STRAIN-KI2 / MGIG55;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                           Escherichia coli.
Bacteria, Proteobacteria, gamma subdivision; Enterobacterlaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                          "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.6%; Score 100; DB 1; Length 307; Best Local Similarity 37.5%; Pred. No. 1; Matches 24; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR000683, GFO_IDH_MOCA.
InterPro, IPR004104, GFO_IDH_MOCA_C.
Pfam; PF01408, GFO_IDH_MOCA, 1.
Pfam; PF02894, GFO_IDH_MOCA, 1.
Virulence; Complete proteome.
SEQUENCE 307 AA; 33681 MW; E8BB622AE0C5C92C CRC64;
                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
          307 AA.
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         PRT;
                                                                                                                                                                                                                                                                                                                  MEDLINE-97061202; PubMed-8905232;
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ID YDGJ_ECOLI STANDARD; F
AC P77376;
DT 15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000207; AAC74152.1; -.
                                                                     Virulence factor mviM homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90743; BAA35876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 3:137-155(1996).
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EcoGene; EG13879; mviM.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AEQK 117
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         MVIM_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makainoto K., Miti T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Salto N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.; A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 IDLIVIPTPNDTHFPLAKAALEAGKHVVVDKPFTVTLSQARELDALAKSLGRVLSVFHINR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHEEHVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
STRAIN=KIZ / MG1655;
STRAIN=P9742617; PubMed=9278503;
Blattiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Garegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Rau B., Shao Y.;
                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coll K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l protein; Oxidoreductase; Complete proteome. 346 AA; 38257 MW; 30F1E436EAC4F3CC CRC64;
16-0CT-2001 (Rel. 37, Last sequence update)
Hypothetical oxidoreductase ydgJ (EC 1....).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.3%; Pred. No. 1.2; tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE000258; AAC74696.1; ALT_INIT.
EMBL, D90805; BAA15375.1; ALT_INIT.
EMBL, D90806; BAA15382.1, ALT_INIT.
EMBL, D90807; BAA15389.1; ALT_INIT.
EMBL, D90808; BAA15319.1; ALT_INIT.
ECOGENE; EG13931; ydgJ.
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InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfan; PF01408; GFO_IDH_MOCA; 1.
Pfan; PF02894; GFO_IDH_MOCA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12;
MEDLINE-97251357; Pubmed-9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                 Escherichia coli.
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226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NTEPERKFGVVVVGVGRAGSVR----ARDLRNPHPSSAFLNLIGFVSRRELG-----SI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=89255091; PubMed=2722750;
Joerger R.D., Jacobson M.R., Bishop P.E.;

"Two nifA-like genes required for expression of alternative
nitrogenases by Azotobacter vinelandii.";

J. Bacteriol. 171:3258-3267(1989).

-:- FUNCTION: ANFA IS ESSENTIAL FOR NITROGEN FIXATION UNDER MO- AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                            J. Ferment. Bioeng. 74.333.344(1992).
-I- FUNCTION: TRANSFORMS 4,5-DIHYDRO-4,5-DIHYDROXYPHTHALATE TO 4,5-DIHYDROXYPHTHALATE.
-I- PATHWAY: SECOND STEP OF PHTHALATE DEGRADATION.
-I- INDUCTION: INDUCED BY PHTHALATE AND REPRESSED BY GLUCOSE.
-I- SIMILARITY: TO ALCALIGENES SP. 1-CARBOXY:3-CHLORO-3,4-DIHYDROXYCYCLOHEXA-1,5-DIENE DEHYDROGENASE.
                                                                                                                                                        Nomura Y., Nakagawa M., Ogawa N., Harashima S., Oshima Y.; "Genes in PHT plasmid encoding the initial degradation pathway phthalate in Pseudomonas putida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 DGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSL 104
                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Azotobacter.
30-MAY-2000 (Rel. 39, Last annotation update)
Putative 4,5,-dihydroxyphthalate dehydrogenase (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 100; DB 1; Length 410; 29.2%; Pred. No. 1.5; ative 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid; Oxidoreductase; Aromatic hydrocarbons catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODIA95B019DCAC1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000683; GFO_IDH_MOCA..
InterPro; IPR004104; GFO_IDH_MOCA_C.
Pfam; PF01408; GFO_IDH_MOCA.1.
Pfam; PF02894; GFO_IDH_MOCA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nitrogen fixation protein anfA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 AA; 45644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13229; BAA02512.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azotobacter vinelandii.
                          (DHP dehydrogenase).
                                                    Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 33; Conserv
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                             STRAIN-NMH102-2
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                                                                                                     NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|: || :: | | :: | 363 LVEMVEQCIFREDLYYRLNVFPITVPPLRERGSDVIALADHFVSAFSRENGKNVKRISTP 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 TEEEKKRGIYAVGEGITGKVVETGKAIVARRLQEHPDFLGRTRVSRNGKAKAAFFCVPIM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNAGKHVLVE------YPMTLSLAAAQELWEL----AEQKGKVLHEEHVELLMEE 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A DOMAIN. SIGMA-54 FACTOR INTERACTION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                       618
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V-DEFICIENT CONDITIONS. IT IS REQUIRED FOR THE REGULATION OF NITROGENASE 3 TRANSCRIPTION. INTERACTS WITH SIGMA-54.
SIMILARITY: 37% IDENTITY TO AZOTOBACTER VINELANDII NIFA AND IDENTITY TO AZOTOBACTER VINELANDII VNFA.
SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 100; DB 1; Length 533; 20.6%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A44514; A44514.

R InterPro: IPR003018; GAF.

R InterPro: IPR002078; Si954_interact.

Pfam; PF01590; GAF; 1.

R Pfam; PF0159; Sigma54_activat; 1.

R PROSITE; PS00675; Sigma54_INTERACT_1; 1.

R PROSITE; PS00675; Sigma54_INTERACT_1; 1.

R PROSITE; PS00675; Sigma54_INTERACT_1; 1.

R PROSITE; PS00689; SiGMA54_INTERACT_1; 1.

R PROSITE; PS00689; SiGMA54_INTERACT_3; 1.

R PROSITE; PS00689; SiGMA54_INTERACT_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-T-H MOTIF.
ODEFBE02A1CF7695 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.1;
51; Mismatches
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319 AT
520 H-
59546 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26751; AAA22146.1; -.
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nes 81; Conservative
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501
533 AA;
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SEQUENCE
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DOMAIN
NP_BIND
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- protein search, using sw model OM protein November 1, 2002, 14:43:58; Search time 31.4084 Seconds Run on:

(without alignments)
905.569 Million cell updates/sec

Title: Perfect score:

US-09-606-129A-3 1508 1 MNTEPERKFGVVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq_length: 0 Maximum DB seq_length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_71:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	biliverdin reducta	biliverdin reducta	biliverdin reducta	biliverdin reducta		dehydrogenase, pro	hypothetical 38.8	probable oxidoredu	probable regulator	probable regulator	hypothetical prote	3-chlorobenzoate-3	probable inositol	hypothetical prote	hypothetical prote	oxidoreductase hom	lipopolysaccharide	Oxidoreductase - f	hypothetical prote	oxidoreductases ho	oxidoreductase ypj	hypothetical oxido		hypothetical prote	conserved hypothet	oxidoreductase hom	oxidoreductase hom	oxidoreductase (EC	hypothetical prote
	ΔΙ	G02066	S62624	A42268	AF2324	S74645	F90486	C65140	AH0994	A91165	A86011	D69803	н69216	A71443	AE2337	AC2319	AE1119	B72359	T39296	S75555	A11428	B86819	T38428	T42744	D71201	670026	AH1479	AH1470	AE3650	F89784
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	Query Match Length	296	296	295	322	328	371	345	345	345	345	393	318	364	374	356	338	360	368	371	343	324	369	352	371	358	338	323	324	346
æ	Query	100.0	8.86	82.7	14.8	14.4	10.4	10.0	10.0	8.6		9.5	•	9.1						•		9.8	•	•	•	•	•		•	8.1
	Score	1508		1247.5	. 222.5	_	157.5	151.5	150.5	147.5	147.5	143	141	136.5	136.5	134	133	132	130.5	130.5	130	129.5	124.5	123.5	123.5	122.5	N		121.5	121.5
	Result No.	П	7	e	4	S	9	7	89	6	10	11	12	13	14	15	16	17	1.8	19	20	21	22	23	24	25	26	27	28	29

GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240 

181

qq δλ qq á

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121 LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLF 180

240

S62624
biliverdin reductase (EC 1.3.1.24) - human
biliverdin reductase (EC 1.3.1.24) - human
N.Alternate names: biliverdin IX-alpha reductase
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 28-Oct.-1996 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
C.Accession: S62624; 856622; S29736
R.Maines, M.D.: Polevoda, B.V.: Huang, T.J.: McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A;Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati

30 121 8.0 341 2 A75025 31 119.5 7.9 342 2 H70014 32 118.5 7.9 348 2 AH1802 34 118.5 7.9 348 2 AH1802 35 118.5 7.9 348 2 B97495 36 116.5 7.7 323 2 AF1109 37 115 7.6 358 2 AC1345 39 114.5 7.6 330 2 D98236 40 114.5 7.6 330 2 D98236 41 11.5 7.6 330 2 AR7302 42 112.5 7.4 349 2 AR1715 45 111.5 7.4 349 2 AR1716 47 111.1 1111111111111111111111111111111	NADH-dependent dyh conserved hypothet oxidoreductases ho dehydrogenase Atul D-galactose 1-dehy oxidoreductase ycg oxidoreductase hom oxidoreductase hom oxidoreductase hom myo-inositol 2-deh myo-inositol 2-deh conserved hypothet oxidoreductase (EC NADH-dependent deh oxidoreductase (EC	NMENTS an eductase 6-Jun-1997 #text_chang guchi, T.; Tomita, M. st 1995 B/EMBL/DDBJ 43231; PID:g1143232	tch 100.0%; Score 1508; DB 2; Length 296; al Similarity 100.0%; Pred. No. 1.1e-109; 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MNTEPERKEGVVVVGVGRAGSVRMFDLRNPHPSSAFLNLIGFVSRRELGSIDGVQOISLE 60 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
30 121 8.0 341 2 31 119.5 7.9 348 2 32 118.5 7.9 348 2 34 118.5 7.9 348 2 34 118.5 7.9 348 2 35 118.5 7.9 308 2 36 116.5 7.7 323 2 37 115.5 7.6 330 2 40 114.5 7.6 330 2 41 112.5 7.6 330 2 42 112.5 7.6 330 2 42 112.5 7.6 330 2 42 112.5 7.4 349 2 43 111.5 7.4 349 2 44 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 349 2 45 111.5 7.4 34	A75025 AH18014 AH2713 AH2713 AH2713 E97495 AF1109 AF1715 AF1715 AF1715 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 AF3004 A	ALI pha ion Yam Aug rom	; SCOTE ; Pred. 0; Mism 0; Mism RMRDLRNP!           RMRDLRNP!
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		RESULT 1 G02066 biliver N'Alterr C;Specit C;Deces: C;Acces: R;Komurc Submirte A;Access A;Access A;Resid A;Cross	Query Best 1 Matchr Qy Db Oy Oy (Qy) (A)

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G; Species: Anabaena sp.
A; Note: Anabaena sp.
A; Note: Anabaena sp.
C; Starin PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C; Accession: AF5324
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Ress 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000019; PIDN:BAB75848.1; PID:g17133284; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                             181 GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 ISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 ----IEEKGPGL-KRNRYLSFHFKSGSL------ENVP-NVGVNKNIFLKDQN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 LAQVIYGKGESLWQPERKFEVHGDNGALIFDGDTGFFIQSGESTPVELGTRRGLFAKDTS
                                                                                                 LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLF
                                                                                                                                                                                                                                                                                      241 VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEE1QKYCCSRK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VVGVGRAGSVRARDLRNPHPSSAFL----NLIG------FVSRRELGSIDGVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IVGTGYAAKLR-----AEAFLEDERSHLVAIAGSKLERTQTFAQAYQAEVITGWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 QOKLLHVEHIELLGGLHQALK----QNLDKVGHLFYVRYSTINPQNPAPRKWTYNHAMF
                                                                                                                                                                                                                                                                                                              163 GFPAFSGISRLTWLVSLFGELSLVSATLEERK---EDQYMKMTVCLETEKKSPLSW----
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                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
AF2324
billverdin reductase [imported] - Anabaena sp. (strain PCC 7120)
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biliverdin reductase (EC 1.3.1.24) - Synechocystis sp. (strain N.Alternate names: hypothetical protein s1r1784
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 KGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLF----TAGP---
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ilarity 26.0%; Pred. No. 8.3e-10;
Conservative 52; Mismatches 110
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87; Conserv
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R; Fakhrai, H.; Maines, M.D.
Biol. Chem. 267, 4023-4029, 1992
A; Title: Expression and characterization of a CDNA for rat kidney biliverdin reductase. A; Reference number: A42268; MUID:92156147
A; Accession: A42268
A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                        to this protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                            A;Cross-references: EMBL:X93086; NID:g1246748; PIDN:CAA63635.1; PID:g1246749
A;Accession: S62622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biliverdin reductase (EC 1.3.1.24) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELSLVSATLEERKEDOYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                      A; Molecule type: protein

A; Molecule type: protein

R; Residues: 3-24, X', 26-37, X', 29-36;48-74;228-234;235-248 <MAF>

R; Maines, M.D.; Trakshl, G.M.

Arch. Biochem. Biophys. 300, 320-326, 1993

Arch. Biochem. Biophys. 300, 320-326, 1893

A; Title: purification and characterization of human biliverdin reductase.

A; Reference number: $29736; MUID:93143333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Residues: 1-295 <FAK>
A;Cross-references: GB:M81681; NID:g203177; PIDN:AAA40830.1; PID:g203178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPNVGVNKNIFLKDQNIFVQKLLGQFSEKELAAEKKRILHCLGLAEEIQKYCCSRK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 3-24,'X',26-27,'X',29-36;48-74;228-234;235-248 <MAW>
A;Note: the sequence of peptide 1 from page 323 seems not to belong
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: BVR
C;Keywords: oxidoreductase
C;Keywords: oxidoreductase
F;3-296/Product: biliverdin reductase IX-alpha #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence extracted from NCBI backbone (NCBIP:82800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.8%; Score 1490; DB 2;
98.6%; Pred. No. 2.7e-108;
iive 2; Mismatches 2;
A; Reference number: S62622; MUID:96202961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: sequence extracted from NC C; Keywords: liver; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: kidney
                                              Molecule type: mRNA
Residues: 1-296 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local Simi
Matches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Matches 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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PCC 6803)

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hypothetical 38.8 kD protein in gntR-ggt intergenic region - Escherichia coli (strain cispecies: Escherichia coli (cispecies: Cista) (cispecies: Cispecies: Cisp
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A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH0994
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VEDTAVAIMR-----YKNGALGTISQTVSMKPTTYQYRKIRVNGSNGFVEITDGS 286
                                                                                                                                                                                                                                                                                                                                                153 TAGPLEEERFGFPAFSGISRLTWLVSLFGELSLVSATLEERKEDOYMKMTVCLETEKKSP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | | : | | : | | : | | : | | | : | | | | : | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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             DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQK--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                       ---VELLMEEF-----AFLKKEVVGKDLLKGSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                               190 WRGMWNTEGGCVMTNQCIHTIDLMIWLNGEVEEVSGFVDNLTHDG-----IE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13;
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1larity 31.3%; Pred. No. 0.0003;
Conservative 27; Mismatches 52;
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C;Superfamily: conserved hypothetical protein b1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | : | : | CSTVAIEGKIEESKSSVEYKK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 IFVQKLLGQFSEKELAAEKKR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGVHTMDQIISLFG 188
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Best Local S
Matches 42
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: F90486
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffrites, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrette to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Reference number: A99139
A;Residues: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-371 <KUR>
A;Cross-references: GB:AE006641; NID:g13816451; PIDN:AAK43149.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                   A;Accession: $74645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <KAN>
A;Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAA16797.1; PID:d101753
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Keywords: oxidoreductase
                                       C;Accession: S74645
KRaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                         A: Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | |: | : | : | : | : | : | 249 TLHGDRGTLIFVGETGRLIQGQTETEITVGSRRGLFRQDTEAVLDYLT---TGKPLYVDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 DPEIDLVLIATINQLHGAIAEAALQAGKHVVLEYPLALTYAMGKKLQOLAREKGKLLHVE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVELLMEEFAFLKKEV--VGKDL-LKGSLLFTAGPLEE-----ERFGFPAFSGISRLTW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 LVSLFGELSLVSATLE--ERKEDQYMK---MTVCLETEKKSPLSWIEEKGPGLKRN-RYL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVVGVGRAGSVRARDLRNPHPSSAFLNLIGFVSRRELGSID-----GVQ-QISLEDALS 64
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19.9%; Pred. No. 0.00011;
tive 58; Mismatches 118;
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A;Reference number: S74322; MUID:97061201
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Gaps

Indels 13;

53; DB 2;

Length 345;

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A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A86011

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <-STO>

A;Coss-references: GSTO>

A;Coss-references: GSTO>

A;Coss-references: GSTO>

A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAG-----PLEEERFGFP---AF-- 167
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                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 147.5; DB 2. Best Local Similarity 30.6%; Pred. No. 0.00061; Matches 41; Conservative 27; Mismatches 53.
                                                                                                                                                                                                                     A;Gene: yhhX
C;Superfamily: conserved hypothetical protein b1624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable regulator [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952 C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: A91165 R; Hayashl, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Status: preliminary A; Shilasha Special Richard A; Status: preliminary A; Molecule type: DNA A; Residus: 1-345 CHAY>
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F; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
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C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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                                                                    A; Residues: 1-345 - CPAR>
A; Residues: 1-345 - CPAR>
A; Cross-references: GB:AL513382; PIDN:CAD08084.1; PID:g16505063; GSPDB:GN00176
C; Genetics:
A; Gene: STY4266
C; Superfamily: conserved hypothetical protein b1624
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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30.6%; Pred. No. 0.00061;
tive 27; Mismatches 53;
                                                                                                                                                                                                                     10.0%; Score 150.5; DB 2; 32.6%; Pred. No. 0.00036;
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C,Superfamily: conserved hypothetical protein b1624
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Best Local Similarity 30.6%
Matches 41; Conservative
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                                                                                                                                                                                                                                           Similarity
                               A; Status: preliminary
A; Molecule type: DNA
       A; Accession: AH0994
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                                                                                                                                                                                                                        Query Match
Best Local
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C;Species: G;Species: G;Specie
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTMFAEEAKRQDGIEVVSIATPNGTHYEICKAALEAGVHVICEKPLFFTSAEGQEIKALA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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6; Conservative 52; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97; Indels
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	C.; Chalwatzis, N. A.Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t A.Reference number: A71400; MuID:98121113 A.Accession: A71443 A.Accession: A71443 A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Residues: preliminary; nucleic acid sequence not shown; translation not shown A.Residues: 1-364 <bev> A.Cross-references: GB:297343; NID:92245073; PID:e327057; PID:92245096 C.Genetics: A;Map position: 4COP9-4G3845</bev>
RESULT 12 H69216 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein - Methanobacterium thermogutorobenzoate-3,4-dioxygenase dyhydrogenase related protein - Methanobacterium thermogutorophicum C;Species: Methanobacterium thermogutorrophicum C;Species: Methanobacterium thermogutorrophicum C;Species: Methanobacterium thermogutorrophicum C;Species: Methanobacterium thermogutorrophicum C;Accession: H69216 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; G;Accession: H69216 A;Specieraca, R.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A;The: Complete genome sequence of Methanobacterium thermogutotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514 A;Reference number: A69000; MUID:98037514 A;Reference number: A69000; MUID:98037514 A;Residues: 1-318 <ath> A;Residues: 1-318 <ath> A;Reperimental source: strain Delta H C;Genetics: A;Experimental source: strain Delta H A;Start codon: TTG C;Superfamily: Streptomyces griseus strI protein</ath></ath>	Query Match         9.1%; Score 136.5; DB 2; Length 364;           Best Local Similarity 23.1%; Pred. No. 0.0047;         1.0047;           Matches         61; Conservative 49; Mismatches 89; Indels 65: Gaps 13;           QY         8 KFGVVVG-VGRAGSVRRDLR
Query Match         9.4%; Score 141; DB 1; Length 318;           Best Local Similarity         20.1%; Pred. No. 0.0018;           Matches         56; Conservative 49; Mismatches 90; Indels 84; Gaps 8;           Qy         7 RRFGVVVGGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDAL 63           1   1   1   1   1   1   1   1   1   1	protein all4252 [imported] - Anabaabaena sp. ca as sp. c
SULT 13  SULT 13  Dable inositol 2-dehydrogenase - Arabidopsis the Species: Arabidopsis thaliana (mouse-ear cress)  Sariety: columbia Date: 03-Aug-1998 #sequence_revision 03-Aug-1998  Accession: A71443  Bancroft, I.; Bent, E.; Love, K.; Goc.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzene anagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Authors: Mueller-Auer, S.; Silvey, M.; James, R. hoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.;	Dest Local Similarity 21.8%; Score 1.00.0049; Matches 49; Conservative 38; Mismatches 77; Indels 61; Gaps 6; Matches 49; Conservative 38; Mismatches 77; Indels 61; Gaps 6; Matches 49; Conservative 38; Mismatches 77; Indels 61; Gaps 6; Matches 49; Conservative 38; Mismatches 77; Indels 61; Gaps 6; Matches 49; Conservative 38; Mismatches 77; Indels 61; Gaps 6; Matches 61; Mismatches 77; Indels 61; Gaps 6; Matches 62; Mismatches 77; Indels 62; Matches 63; Matches 63; Matches 64; Mismatches 64; Mismatches 64; Mismatches 64; Mismatches 64; Mismatches 65; Matches 64; Mismatches 66; Mismatch

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Cispecies: Anabaena sp.
Anabaena sp.
Anabaena sp.
Anabaena sp.
Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
CiDate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
CiAccession: AC2319
KiAnako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001; Sugimoto, M.; Takazawa, M.; Vamada, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AC2319
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: DNA
A; Residues: 1-356 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75805.1; PID:g17133241; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: all4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 IDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 VVVVGVGRAGSVRMRD------LRNPHPSSAFL-----NLIGFVSRRELGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Indels 52; Gaps
                                                                                                                                                                                       hypothetical protein all4106 [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 WELAEQKGKVLHEEHVELL---MEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 134; DB 2; Length 356; 24.9%; Pred. No. 0.0071; tive 28; Mismatches 53; Indels
180 FGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWI--EEKGPG 222
                               | :| :| |
|-----RPWNWYSSKEKGG 184
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Best Local Similarity 24.9%
Matches 44; Conservative
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                                                     166 RADTS----
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Search completed: November 1, 2002, 14:50:55 Job time : 32.575 secs

us-09-606-129a-3.rai

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APPI
APPII
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1, Appli
519, App
15, Appl
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                                                                                                                                                (without alignments)
292.168 Million cell updates/sec
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                                                                                                                      1, 2002, 14:44:48; Search time 24.746 Seconds
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1508
1 MNTEPERKFGVVVVGVGRAG.....RILHCLGLAEEIQKXCCSRK
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-720-817-6
US-09-720-817-1
US-09-936-165A-519
US-09-376-700-15
US-08-286-819A-19
US-08-286-819A-19
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US-08-712-700-18-0
US-08-712-700-18-0
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US-09-330-330-1
US-08-745-934-4
US-09-147-009-7
US-08-852-743-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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28 61.5 5.4 222 1 US-07-992-6270-1 Sequence 1 29 61.5 5.4 222 1 US-07-992-6270-1 Sequence 1 20 61.5 5.4 222 1 US-08-246-993-1 Sequence 1 20 61.5 5.4 222 1 US-08-246-993-1 Sequence 1 20 61.5 5.4 222 1 US-08-746-993-2 Sequence 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Sequence 1, Appl1 Sequence 1, Appl1 Sequence 3, Appl1 Sequence 3, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 3, Appl1 Sequence 3, Appl1 Sequence 6, Appl1 Sequence 6, Appl1 Sequence 11, Appl1 Sequence 6, Appl1 Sequence 69, Appl	AND SECRET CARRYING THE SAME 0,817 03200 3410 123.5; DB 4; Length 315; NO. 6.9e-05; smatches 136; Indels 75; Gaps 12; smatches 136; Indels 75; Gaps 12; smatches 136; Indels 75; Gaps 12; HVLVEY PWTLSLAAAOELWELAEQKGKVLHE 123 HVLVEY PWTLSLAAAOELWELAEQKGKVLHE 123 HVLVEY PWTLSLAAAOELWELAEQKGKVLHE 123 HVQVEIPLABSWADAEAVWKKSOFTGLVCWV 118 HYQVEIPLABSWADAEAVWKKSOFTGLVCWV 118 HAQPLEEERFGFPAFSG 169 1
28 29 30 30 31 31 31 31 32 33 34 44 44 44 44 44 44 44 44 44 44 44	US-07-992-827D-1 US-08-216-593-1 US-08-216-593-1 US-09-147-009-6 US-09-09-147-009-6 US-09-503-391-2 US-09-517-82-2 US-09-417-822-2 US-09-517-822-2 US-09-517-822-2 US-09-517-822-2 US-09-517-822-2 US-09-517-822-2 US-08-557-210A-3 US-08-557-210A-3 US-08-557-210A-4 US-08-6854-695-2 US-08-854-854-699 US-08-951-843A-69 US-08-951-843A-69 US-08-951-843A-69	20817  TO  TO  TO  TO  TO  TO  TO  TO  TO  T
28 29 30 30 31 31 31 31 32 33 34 44 44 44 44 44 44 44 44 44 44 44	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	pplication US/097 (U5579  MATION: Isai, Eiji  Wikuda, Masao (atayama, Yoshihi  dishikawa, Seiji  dotta, Yasushi  fotta, Yasushi  fotta, Yasushi  fotta, Yasushi  fotta, Yasushi  fotta, Yasushi  MIDON NUMBER: Doll-06  WICOATION NUMBER: Porl  DATE: 1998-06-25  VID NOS: 10  ID NOS: 10  centin Ver. 2.1  conservative  MGAGGEKHLDGLKNIDG  SVAICSESSSHEDYIF  AGAGGEKHLDGLKNIDG  SVAICSPTOMMAEQAI  MEEFAFLKKEVVGKDI  MEEFAFLKKEVVGKDI  MATION NUMBER: Porl  AGAGGEKHLDGLKNIDG  SVAICSPTOMMAEQAI  MEEFAFLKKEVVGKDI  MEEFAFLKKEVGVGKDI  MEEFAFLKKEVGVGKDI  MEEFAFLKKEVGKDI  MEEFAFLKKEVGKDI  MEEFAFLKKEVGKDI  MEEFAFLKKEVGKU  MEEFA
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170 ISRLTW-----LVSLFG----

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207 TEKKSPLS----WIEEKGPGLKRNRYLSFHFKSGSLE--NVPNVGVNKN-IFLKDQNIFV 259 

167 TDHLLWHHAAHTVDLFAYQAGKIVQANAVQGPIHPELGIAMDMSIQLKSETGAICTLSLS

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64 SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 122.5; DB 4; Length 280; Pred. No. 7.4e-05; 33; Mismatches 66; Indels 11
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SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: JAPAN 10/203200
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PCT/JP99/03410
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
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FILING DATE: 24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Sphingomonas sp. CR-0310201
PUBLICATION INFORMATION:
US-09-720-817-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 519, Application US/08936165A; Patent No. 6348582
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APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 EHVELLMEEFAFLKKEVVGKDL 145
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicholas, Richard
Pratt, Julie
Reichard, Richard
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Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.118
Best Local Similarity 22.55
Matches 32; Conservative
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CITY: King of Prussia
STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Black,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-936-165A-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HAPPLICANT: APPLICANT: APPLICANT: NAPPLICANT: NAPPLICANT: HAPPLICANT: NAPPLICANT: NAPPLICAN
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                                                                                                                                                                                                                                                                                  LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                  SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GHTRRFNPSHQYIHNKIV------AGELAIQQMDVQTYFFRRKNMNAKGEPRSW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 IDHLLWHHAAHTVDLFAYQAGKIVQANAVQGPIHPELGIAMDMSIQLKSETGAICTLSLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 TEKKSPLS----WIEEKGPGLKRNRYLSFHFKSGSLE--NVPNVGVNKN-IFLKDQNIFV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 SSQEVEVAYICSESSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 IALAGAGAFGEKHLDGLKNIDG----VEIVSIISRKAEQAAEVAAKYGAKHSGTDLSEAL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL 63
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Katayama, Yoshihiro
APPLICANT: Katayama, Yoshihiro
APPLICANT: Nishikawa, Seiji
APPLICANT: Hotta, Yasushi
TITLE OF INVENTION: NOVE GENE AND TRANSFORMANT CARRYING THE SAME
FILE REFERENCE: 200966USOXPCT
CURRENT APPLICATION NUMBER: 02/09/720,817
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: PCT/JP99/03410
PRIOR FILING DATE: 1999-07-17
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
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APPLICANT: Fukuda, Masao
APPLICANT: Fukuda, Masao
APPLICANT: Katayama, Yoshihiro
APPLICANT: Nishikawa, Seiji
APPLICANT: Hotta, Yasushi
TITLE OF INVENTION: NOVEL GENE AND TRANSFORMANT CARRYING THE SAME
TITLE OF SOUSONOVEL 20096GUSOXPOT
CURRENT APPLICATION NUMBER: US/09/720,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 EHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 123.5; DB 420.0%; Pred. No. 6.9e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                           283 AIREGREPNSSVA----RVLDCYRVLGELE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AIREGREPNSSVA----RVLDCYRVLGELE 308
   260 QKLLGQFSEKELAAEKKRILHCLGLAEEIQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 OKLLGOFSEKELAAEKKRILHCLGLAEEIQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Sphingomonas sp. CR-0310201 US-09-720-817-6
                                                                                                                                                                                                   5-09-720-817-6
Sequence 6, Application US/09720817
Patent No. 6340579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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Patent No. 6340579
GENERAL INFORMATION:
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APPLICANT: Fukuda, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 66; Conserv
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101 TTASDTARLVGLARRKNLLLRENYL-----FLHHGRHDVVRDLLQ-----SGEIGELR 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 LSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEER 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 -----FGFPAF--SGISRLTWLVS--------LFGELSLVSATLEERKEDQ 197
                                                                                                                                                                                                                                                  102 LSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEER 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 FVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWT 101
                                                                                                                                                            42 FVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMT 101
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Erawford, Kathryn P
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
ITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
ITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.4%; Score 112; DB 4; Length 332; Best Local Similarity 24.5%; Pred. No. 0.0012; Matches 47; Conservative 34; Mismatches 69; Indels
                                                                         Length 332;
                                                                                                                 69; Indels
                                                                     ; Score 112; DB 4;
; Pred. No. 0.0012;
34; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Saccharopolyspora spinosa US-09-370-700-15
                                                                       Query Match
Best Local Similarity 24.58;
                                                                                                                 Matches 47; Conservative
  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             : :| |::|
209 VDLSGSVLLQSE 220
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209 VDLSGSVLLQSE 220
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US-09-036-987A-15
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US-08-286-819A-19
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US-09-370-700-15
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                                                                                                                                                                                                                                                                                                                                                                                     54 LKDDTIDVIHVCTPNDSHCEITVAGLHAGKHVWCEKPWAKTTAEAQKMIDIAKSTGKKLT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 EEHVELLMEEFAFLKKEVVGKDLLKGSLLF------TAGPL--EEERFGFPAFS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 IGYONRFRPDSQFLHQAAQRGDL--GDIYFGKAHAIRRRAVPTWGVFLNEEAQGGGPLID 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GISRLTWLVSLFGELSLVSATLEERKEDQYMKMTVCLETEKKSPLSW 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 IGTHALDLTLWMMDNYEPESVMGSTFHK------LNKQHDAPNAW 210
                                                                                                                                                                                                                                                                       7.4%; Score 112; DB 4; Length 229; 22.8%; Pred. No. 0.0007;
tive 30; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
ELLOATION NUMBER: US/09/036,987A FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/MOCKET NUMBER: 50,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                TELEX:
INPORMATION FOR SEQ ID NO: 519
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 332 amino acids
TYPE: amino acid
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                       Ouery Match 7.48
Best Local Similarity 22.88
Matches 39; Conservative
                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: Protein US-08-936-165A-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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ALFULCANT: COUNTAIN PATRICE
TITLE OF INVENTION: PATRICES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON. COUNTY
ADDRESSEE: OBLON.
: | | :::| |: ::| |: |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |: ::| |:
                                                                                                                                                                                                                                     241 VPNVGVNKNIFLK-------DQN-----IFVQKLLGQFSEKELAAEKKR 277
                                                                                                      196 DQYMKMTVCLETE----KKSPLSWIEEKGPG------LKRNRYLSFHFKSGSLEN
                                                                                                                                                                  191 EQKEKLEGIITSQHPSESNKTILGWLKEP-PGHPSPETFLKIIERLEYI----RGMDLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION 0ATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 38-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTONNEY/AGENT INFORMATION:
NAME: Oblon, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/980,357 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08980357
Patent No. 6013508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DOKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               278 ILHCLG----LAEEIQK 290
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amino acid
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COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                   152 LRK---
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                                                                                                                                                APPLICANT: MOLINAS, CATHERANDE IMPLICATED IN THE TITLE OF INVENTION: PATRICE TITLE OF INVENTION: PAPPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 LKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLFGELSLVSATLEERKE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SVRMRDLRNP-----HPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICS 75
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION UNMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
FILING DATE: 31-OCT-1990
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
Sequence 19, Application US/08286819A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
                                                                                           ARTHUR, MICHEL
DUKTA-MALEN, SYLVIE
MOLINAS, CATHERINE
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TELEFAX: (703) 413-2220
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Best Local Similarity 20.8%;
...rohes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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                                                                                                                                      APPLICANT
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67 -- ELDKLQQKEEQAERLVKQL-EEEAKSRAEELKLLEEKLKGKEAELEKSSAAHTQATLL 123
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                                                                                                                                                                                                                                                                                                                                                                                                           EEERFG------FPAFSGISRLTWLVSLFGELSLVSATLEER-------193
                                                                                                                                                                                                                                                                                                                                        124 LEEKYDSMVOSLEDVTAQFESYKALT--ASEIEDLKLENSSLQEKVAKAGKNAEDVOHQI 181
                                                                                                                         54 VQQISLE-DALSSQEVEVA----YICS-----ESSSHEDYIRQFLNAGKHVLVEYPM 100
                                                                                                                                                                                                             101 TLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGK - DLLKGSLLFT - AGPL 157
                                                                                                                                                   ; Score 92.5; DB 1; Length 351;
; Pred. No. 0.15;
39; Mismatches 85; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilbamer, Jeffrey J.
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 ----LKQQEEDFRKQLEDEEGRKAEKENTTAE------LTEEINKW 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 NIFLKDONIFVOKLL ---- GQFSEKELAAEKKRILHCLGLAEEIQKY 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF-0028-1 DIV
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FILING DATE: August 20, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08700178
Patent No. 5783669
Patent No. 5783669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                     Query Match
Best Local Similarity 25.1%;
Matches 72; Conservative 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: CA
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US-08-402-217A-2
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US-08-700-178-2
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                                                                                                                                                                                                                                                                                                                                        136 LKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLFGELSLVSATLEERKE 195
                                                                                                                                                                                                                                                                                                                                                                                                                            196 DQYMKMTVCLETE-----KKSPLSWIEEKGPG------LKRNRYLSFHFKSGSLEN 240
                                                                                                                                                                                                ESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAF 135
                                                                                                                                                                                                                                                                                 152 LRK-------NKIILPAITTLERMVWEARAMAEKKLFNTVSKSLTN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DQN-----IFVQKLLGQFSEKELAAEKKR 277
                                                                                                                                                                   21 SVRMRDLRNP-----HPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICS 75
                                                                                                                           96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2., Application US/08402217A
Patent No. 5587301
GENERAL INFORMATION:
APPLICANT: Hawfins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
                                                                                 DB 3; Length 988;
                                                                             Ouery Match 6.4%; Score 97; DB 3; Length 988 Best Local Similarity 20.8%; Pred. No. 0.25; Matches 66; Conservative 49; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: INCYTE PHARMACEUTICALS, INC 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/402,217A FILING DATE: 10-MAR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-852-0195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 3395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 ILSLLSKGRKAQEEIQK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPNVGVNKNIFLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 ILHCLG----LAEEIQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
STREET: 3174 POrter
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                   MOLECULE TYPE: protein
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palo Alto
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                                       US-08-980-357-19
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Query Match
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                                                                                                                                                                                                                                                  EEERFG------FPAFSGISRLTWLVSLFGELSLVSATLEER------- 193
                                                                               54 VQQISLE-DALSSQEVEVA----YICS-----ESSSHEDYIRQFLNAGKHVLVEYPM 100
                                                                                                                                                                 101 TLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGK - DLLKGSLLFT-AGPL 157
                                                                                                                                                                                                                                                                                       124 LEEKYDSMVQSLEDVTAQFESYKALT -- ASEIEDLKLENSSLQEKVAKAGKNAEDVQHQI 181
                                                                                                                                                                                                                                                                                                                                  ----KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVNK 248
                                                                                                           6.1%; Score 92.5; DB 1; Length 351; 25.1%; Pred. No. 0.15; tive 39; Mismatches 85; Indels 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig
APPLICANT: Selinaer, Jeffrey
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
                                                                                                                                                                                                                                                                                                                                                                                                                                         227 ----LKQQEEDFRKQLEDEEGRKAEKENTTAE------LTEEINKW 262
                                                                                                                                                                                                                                                                                                                                                                                                                 249 NIFLKDQNIFVQKLL----GQFSEKELAAEKKRILHCLGLAEEIQKY 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPPERAING SYSTEM: Windows
OPERAING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,654
FILING DATE: December 22, 1997
CLASSIFICATION 14 35
PRIOR APPLICATION NUMBER: 08/700,178
FILING DATE: Angust 20, 1996
PRIOR APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
ATTOMNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0028-2 DIV
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US-08-995-654-2
; Sequence 2, Application US/08995654
; Patent No. 6025138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: Linear, US-08-995-654-2
                   Local Similarity
nes 72; Conserv
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  Query Match
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                                                                                                                                                                                                                                                                                         101 TLSLAAAQELWELAEQKGKVLHEEHVELLMEEFAFLKKEVVGK--DLLKGSLLFT-AGPL 157
                                                                                                                          158 EEERFG------FPAFSGISRLTWLVSLFGELSLVSATLEER------
                                                                                                                                                                                                                                                                                                                                                ----KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNVGVNK
                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114 CORRESPONDENCE ADDRESS: ADDRESSE: Steven & T. STREFFF.
                 Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 ---LKQQEEDFRKQLEDEEGRKAEKENTTAE-----LTEEINKW 262
                                                                                                                                                                                                                                                                                                                                                                                                                                249 NIFLKDONIFVOKLL----GOFSEKELAAEKKRILHCLGLAEEIOKY 291
               Score 92.5; DB 3;
Pred. No. 0.15;
6.1%; Scc...
25.1%; Pred. No. v...
... 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: Protein kinase; Table 8 Column 9 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MacIntosh 7.0 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/857,224B FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Hunter, T.
TITLE: The protein kinase family TOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Steven A. Benner
Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple MacIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                       Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                  Best Local Similarity
Matches 72; Conserv
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APPLICANT: Benner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Hadlau
CITY: Zurich
STATE: none
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US-07-857-224B-9
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150 LLFTAGPLEEE-RFGFPAFSGISRL-----TWLVSLFGELSLVSATLEERKEDQYMKMT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYIRQFLNAGKHVLVEYPMTLSL-AAAQELWELAEQKGK-----VLHEEHVELLMEEFA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :| || | : || | : :|| || :| || 327 --LPSDVNEGKTVFIR---NLSFDSEEEELGELLQQFGELKYVRIVLHPDTEHSKGCAFA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 VRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHE 81
                                                                                                                                                                   103 -----SLAAAQELWELAEQKGKVLHEEHVELLMEEFA-----FLKKEVVGKDLLKGS
                                                                                                                                                                                                                                                                           1 MNTEPERKFGVVVVGVGRAGSVRMRDLRN------PHPSSAFLNLIGFVSRRELG
                                                                                    50 SIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTL.....
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                                                                                                                                                                                                                                                                                                                                                         352 EVIHVSGKDHASYYPEATDILLK---LIFHPETGEIYGAQGVGAKGVDKRI 399
                                                                                                                                                                                                                                                                                                                              203 VCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLENVPNV---GVNKNI 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                          144 LEKOPKR---AVIVGAGFIGLEMAENLKRRGLEVMVIEQAPH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 1;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Science & Technology Law Group 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08676967
Patent No. 5747317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 268 Busn Strancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   55 I-----MQGAHSDFIVRLYRTFKDSKYLY-MLMEACLGGELWTILRDRGSFEDSTTRF 106
                                                                                                                                                                                                                                             68 VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWTLSLAAAQELWELAEQKGKVLHEE--- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                             Gaps
                                                                                                                                                                                          9 FGVV-VVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COENZYME A DISULFIDE REDUCTASE,
TITLE OF INVENTION: AND INHIBITORS THEREOF USEFUL AS ANTIMICROBIAL
TITLE OF INVENTION: AGENTS
UNMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                              125 HVELLMEEFAFL-KKEVVGKDLLKGSLLFT-AGPLEEERFGFPAFSGISRLTW 175
                                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%; Score 90; DB 3; Length 551; Best Local Similarity 22.3%; Pred. No. 0.56; Matches 65; Conservative 43; Mismatches 107; Indels
                                                                                6.0%; Score 91; DB 2; Length 264;
22.5%; Pred. No. 0.14;
tive 33; Mismatches 79; Indels
                                                                                                                      79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COMPALLALE
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,886
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6016.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Katz, Leonard
APPLICANT: Delcardayre, Stephen B.
APPLICANT: Davies, Julian E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08886886
Patent No. 6107068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 551 amino acids
                                                                                                     Best Local Similarity 22.5
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Casuto, Dianne REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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APPLICANT: Katz, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-886-886-15
                                        US-07-857-224B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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STATE:
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135 -FLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLFGELSLVSATLEER 193
                                                                                                  194 KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFH--FKSG--SLENVPNVGVN-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYIRQFLNAGKHVLVEYPMTLSL-AAAQELWELAEQKGK-----VLHEEHVELLMEEFA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISRLTWLVSLFGELSLVSATLEER 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 KEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFH--FKSG--SLENVPNVGVN-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVAYICSESSSHE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9%; Score 89; DB 1; Length 759; Best Local Similarity 21.5%; Pred. No..1.2; Matches 56; Conservative 44; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                              ...o. 08-676-974-1
; Sequence 1, Application US/08676974
; Patent No. 5770422
; GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group STREE: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 QFMTQEAAQKCLLAASPENEAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/CDCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS:
                        |: ||||||| :
467 ERFELLKHQKLKDQNIFVSR 486
                                                                                                                                                        248 -----KNIFLKDQNIFVQK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: not relevant : MOLECULE TYPE: peptide US-08-676-974-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Search completed: November 1, 2002, 14:51:55 Job time: 25.746 secs
                     |: ||||||| : 467 ERFELLKHQKLKDQNIFVSR 486
δ
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248 -----KNIFLKDQNIFVQK 261

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

1, 2002, 14:40:53 ; Search time 67.0997 Seconds
 (without alignments)
 489.985 Million cell updates/sec November Run on:

Title: Perfect score:

US-09-606-129A-3 1508 1 MNTEPERKFGVVVVGVGRAG......RILHCLGLAEEIQKYCCSRK 296 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 segs, 111073796 residues Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_032802:

/SIDSI/gcgdata/geneseq/geneseqp-emb1/An1980.DAT:*
/SIDSI/gcgdata/geneseqy-emb1/An1981.DAT:*
/SIDSI/gcgdata/geneseqy-emb1/An1981.DAT:*
/SIDSI/gcgdata/geneseqy/geneseqp-emb1/An1983.DAT:*
/SIDSI/gcgdata/geneseqy/geneseqp-emb1/An1983.DAT:*
/SIDSI/gcgdata/geneseqy/geneseqp-emb1/An1985.DAT:*
/SIDSI/gcgdata/geneseqy/geneseqp-emb1/An1985.DAT:*
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/SIDSI/gcgdata/geneseqy/geneseqp-emb1/An1988.DAT:*
/SIDSI/gcgdata/geneseqy-emb1/An1989.DAT:*
/SIDSI/gcgdata/geneseqp-emb1/An1989.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA197.DAT:* /SIDS1/gcgdata/geneseg/genesegp-emb1/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:* /SIDS1/gcgdata/geneseq/geneseap.embl/AA1992./SIDS1/gcgdata/geneseq/geneseap.embl/AA1993.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Human secreted pro	Human secreted pro	Novel human diagno	Novel human diagno	Novel human diagno	Drosophila melanod	Propionibacterium	Amino acid sequenc	Sphingomonas sp. C	Sphingomonas sp. C	Putative P. abyssi
	ID	AAG02024	AAG02023	ABG21584	ABG21582	ABG29497	ABB60024	AAU49252	AAW28328	AAY 68460	AAY 68459	AAB96416
		21	21	22	22	22	22	22	18	21	21	22
	Query Match Length DB	09	63	434	241	389	335	226	175	315	280	341
æ		14.9	12.1	10.0	9.7	9.7	8.7	8.3	8.2	8.2	8.1	8.0
	Score.	225	182	151.5	147	147	130.5	124.5	123.5	123.5	122.5	121
	Result No.	п	7	Э	4	S	9	7	8	6	10	11

Staphylococcus aur	Corynebacterium ql	Staphylococcus aur	Glucose-fructose o	SpnN protein invol	S. spinosa protein	Micromonospora eve	Staphylococcus aur	Staphylococcus aur	Putative P. abyssi	Group B Streptococ	Streptomyces galil	Propionibacterium	E. coli growth and	Propionibacterium	Mycobacterium tube	Human male enhance	C glutamicum prote	Corynebacterium gl	Transposase from g	Propionibacterium	H. pylori GHPO 138	Novel human diagno		S	S		Arabidopsis thalla	Arabidopsis thalla	Putative P. abyssi	C glutamicum prote	Corynebacterium ql	Drosophila melanog
AAU36865	AAB79386	AAU34111	AAW77759	AAY39310	AAB70956	AAU04826	AAU34110	AAU36864	AAB96316	AAU03634	AAE00480	AAU49114	AAG98892	AAU56511	AAG81126	AAB69070	AAG93130	AAB79395	AAR24302	AAU43141	AAW98401	ABG20518	AAG23569	AAG23568	AAG23567	AAG42560	AAG42559	AAG42558	AAB96297	AAG89934	σ	ABB67972
22	7 7 7	22	13	20	22	22	22	22	22	22	22	22	22	22	22	22	22	22	13	22	13	22	21	77	21	21	21	21	22	22	22	22
346	337	341	229	332	336	344	357	359	315	327	329	702	307	4	1316	3	359	359	986	344	219	753	360	363	367	463	467	506	867	341	341	417
7.9	7.7	7.7			7.4		7.4	7.4	7.4	7.3			9.9		•		6.4	6.4			6.3	•	•	•					•		•	•
119.5	116.5	116.5	112	112	112	112	112	112	111.5	110.5	105	102.5	100	99.5	98.5	86	. 97	6	δ	95.5	95	95	4.	94.5	4.	4	4	4.	ω.	93	93	93
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

### ALIGNMENTS

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping. Human secreted protein, SEQ ID NO: 6105. AAG02024 standard; Protein; 60 AA. 06-OCT-2000 (first entry) Homo sapiens. EP1033401-A2 06-SEP-2000. AAG02024; 

21-FEB-2000; 2000EP-0200610.

99US-0122487 26-FEB-1999;

Duclert A, Glordano J; Dumas Milne Edwards J, (GEST ) GENSET

WPI; 2000-500381/45. N-PSDB; AAC02030 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

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us-09-606-129a-3.rag

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18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                      ABG21584;
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                            ABG21584
                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                     The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intect 5' ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                         DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                             Score 225; DB 21; Length 60; Pred. No. 2.1e-14; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              24 MRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRDLRNPHPSSAFLNLXGFVSRRELGSIDGVQQISLEDALSSQEVEV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A, Giordano J;
Claim 13; SEQ ID 6105; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 6104; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein, SEQ ID NO: 6104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG02023 standard; Protein; 63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                               14.9%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                          60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC02029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                            Sequence
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations components.
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DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                            Score 182; DB 21;
Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNAEPERKFGVVVVGVGRAGSVRMRDLRNXHPXSAFLNL 39
                                                                                                                                                                                                                                                                                                                                                                                      1 MNTEPERKFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNL 39
                                                                                                                                                                                                                                                                                                               0; Mismatches
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92.3%;
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2000US-0649167
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Best Local Similarity 92.39
Matches 36; Conservative
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                                                                                                                                                             63 AA;
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23-AUG-2000;
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                    241 AA;
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responsible
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                                                                                                                                59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                   119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAG-----PLEEERFGFP---AF-- 167
                                                                                                                                                                                                                                 204 LTVTPYONRRFDSCFLTAKKAIESGKL--GEIVEVESHFDYYRPVAETKPGLPQDGAFYG 261
                                                                                                    Gaps
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                                                                                                   13;
                                                                   Length 434;
                                                                                                   Indels
                                                                DB 22;
                                                                10.0%; Score 151.5; DB 2
31.3%; Pred. No. 4.3e-06;
ive 27; Mismatches 52
at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #21573.
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2000US-0649167.
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                                                                                                   Conservative
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262 LGVHTMDQIISLFG 275
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                                                                               Local Similarity
les 42; Conserv
                                  434 AA;
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                 Score 147; DB 22;
Pred. No. 5.2e-06;
3; Mismatches 53;
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29.9%; Pred
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2000US-0649167.
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WPI; 2001-616774/71.
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07-JUL-2000;
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequence of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                 Length 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 6864.
                                                                                                                                                                                               9.7%; Score 147; DB 22;
29.9%; Pred. No. 1e-05;
ative 28; Mismatches 53;
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11-JUL-2000; 2000US-0614150.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 LVALVTGLENLENDAVITGTKGEIKLSNYW---CCTQISRSNAPPESW-----PLPRAK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GSIDGVQQISLEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNTEPERKFGVVVVG-----FVGRAGSVRMRDLRNPHPSSAFLNLIG-----FVSRREL- 48
cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 SLGGSILMDIGIYALQLGQFVF----GVSPVKILPSGTQLNKERVDVQIDFMLDYGDGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 LTWLVSLFGEL---SLVSATLEERKEDQYMKMTVCLETEKKS--PLSWIEEKGPGLKRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MOSQANLNWGIAAAGRITQDFVTALGTVE----KSRHVVVAVADVDGQRAQQFAQRNQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                         Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 130.5; DB 22; Length
23.2%; Pred. No. 0.00033;
Lve 43; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhatia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELWELAEQKGKVLHEEHVELLMEEF----AFLKKEVVGK----
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 LLKGSLLFTAG--PLEEERFGFPAFSGIS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU49252 standard; Protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US12865
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                                                                                                                                  (ABB57737-ABB72072).
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WO200004134-A1.
             WO9730070-A1
                                                                                                                                                            Black MT,
                                                                                                                                                                         Pratt JM,
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AAY68460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conjugations and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyellitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies capecific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Consyme linked immunosorbent assay (ELISA).

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 DLPVLPDVDAVIETGIDYCVVAAPTKFHEEIGLKLAEAGVHALIEKPLAYDTAAATRLAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LAEQKGKVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSGISR 172
                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQEVEVA- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of glucose-fructose oxidoreductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residues designated X are not defined in
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 124.5; DB 22; Length 24.4%; Pred. No. 0.00073; tive 20; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                   Claim 6; SEQ ID No 10447; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers Misc-difference 1..175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW28328 standard; Protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 LTWLVSLFGELSLVSATLEER 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                         226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde dehydrogenase; 2-pyrone-4,6-dicarboxylic acid; 3,4-dihydroxybenzoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host gagainst invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Staphylococcus aureus protein, that,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 -----VEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AVETPSELFKLVDAVVICTPNKFHADLSIEALNHGVHVLCEKPMXMTTEECDRMIEAANK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 KFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 KGKVL----HEEHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAFSG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 NHKLLTVAYHYRHTDVAMTAKKAIEAGVVGKPLV-----APLSXRCVGVKXLGG 163
                                                                                                                                                                                                                                                                          Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 123.5; DB 18; Length
Pred. No. 0.00064;
2; Mismatches 77; Indels
                                                                                                                                                                                                                                                                          Knowles DJC,
                                                                                                                                                                                                                                                                                                          Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sphingomonas sp. CR-0310201 CHMSD SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                          Rosenberg M,
                                                                                                                                                                                                                                                                              Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY68460 standard; Protein; 315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 610; 989pp; English.
                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 8.2%; Sc
Local Similarity 26.6%; Pr
nes 47; Conservative 22;
                                                                   97WO-US02318
                                                                                                                                       96US-0011888
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                                                                                                                                                                                                                                                                          Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-424969/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT84223
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                                                                                                                                       20-FEB-1996;
                                                                   19-FEB-1997;
21-AUG-1997
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.. 2: us-09-606-129a-3.rag

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FR2792651-A1.
                                                                         17-JUL-1998;
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                                                     25-JUN-1999;
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                                27-JAN-2000
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                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde dehydrogenase; 2-pyrone-4,6-dicarboxylic acid; 3,4-dihydroxybenzoic acid.
                                                                                                                                                                                                                   The present sequence represents an alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde dehydrogenase (CHMSD) originating in Sphingomonas sp. CR-0310201. CHMSD can be used in the production of 2-pyrone-4,6-dicarboxylic acid by culture of a transformant comprising CHMSD in the presence of a suitable precursor such as 3,4-dihydroxybenzoic acid (which is converted in situ into alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde).
                                                                                                                                                                                                                                                                                                                                                                                                                                124 EHVELLMEEFAFLKKEVVGKDLLKGSLLFTAGPLEEERFGFPAF------SG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHTRRFNPSHQYIHNKIV-----AGELAIQQMDVQTYFFRKNMNAKGEPRSW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ELSLVSATLEERKEDQYMKMTVCLE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 TEKKSPLS----WIEEKGPGLKRNRYLSFHFKSGSLE--NVPNVGVNKN-IFLKDQNIFV 259
                                                                                                                                                     New alpha-hydroxy-gamma-carboxymuconic acid eta-semialdehyde dehydrogenase for industrial production of 2-pyrone-4,6-dicarboxylic
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                     3 IALAGAGAFGEKHLDGLKNIDG----VEIVSIISRKAEQAAEVAAKYGAKHSGTDLSEAL 58
                                                                                                                                                                                                                                                                                                                                                                         11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 TDHLLWHHAAHTVDLFAYQAGKIVQANAVQGPIHPELGIAMDMSIQLKSETGAICTLSLS
                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                                              8.2%; Score 123.5; DB 21; Length 315; 20.0%; Pred. No. 0.0014; ative 53; Mismatches 136; Indels 75;
                                                                                                χ;
                                                                                                Hotta
                                                                                                Nishikawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonas sp. CR-0310201 CHMSD SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 OKLLGOFSEKELAAEKKRILHCLGLAEEIQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AIREGREPNSSVA----RVLDCYRVLGELE 308
                                                                                                                                                                                                Claim 1; Page 26-27; 34pp; Japanese.
                                                                                                Fukuda M, Katayama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY68459 standard; Protein; 280
                     99WO-JP03410.
                                           98JP-0203200
                                                                                                                               N-PSDB; AAZ88148, AAZ88151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 ISRLTW-----LVSLFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                               (MAZN ) COSMO RES INST. (MAZN ) COSMO OIL CO LTD.
                                                                                                                                                                                                                                                                                                                                       Similarity 20.0
56; Conservative
                                                                                                                     WPI; 2000-147784/13
                                                                                                                                                                                                                                                                                                          315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sphingomonas sp
                                           17-JUL-1998;
27-JAN-2000
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                                                                                                Masai E,
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                           Local
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The present sequence represents an alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde dehydrogenase (CHMSD) originating in Sphingomonas sp. CR-0310201. CHMSD can be used in the production of 2-pyrone-4,6-dicarboxylic acid by culture of a transformant comprising CHMSD in the presence of a suitable precursor such as 3,4-dihydroxybenzoic acid (which is converted in situ into alpha-hydroxy-gamma-carboxymuconic acid-eta-semialdehyde).
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ARDDVDAVILCTPTQMHAEQAIACMNAGKHVQVEIPLADSWADAEAVMKKSQETGLVCMV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSOEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKGKVLHE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New alpha-hydroxy-gamma-carboxymuconic acid eta-semialdehyde dehydrogenase for industrial production of 2-pyrone-4,6-dicarboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRR-----ELGSIDGVQQ--ISLEDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 122.5; DB 21; Length 22.5%; Pred. No. 0.0015; ive 33; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                Υ;
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                                                                                                                                                                                                                                                                                                                   Hotta
                                                                                                                                                                                                                                                                                                                Nishikawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 23-25; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative P. abyssi dehydrogenase #9.
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                                                                                                                                                                                                                                                                                                             Katayama Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GHTRRFNPSHQYIHNKIVAGEL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 EHVELLMEEFAFLKKEVVGKDL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CNRS ) CNRS CENT NAT RECH SCI
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Matches 32; Conservative
                                                                                                                                                                                                                                                                                                             Masai E, Fukuda M,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147784/13
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WO200004134-A1
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(MAZN ) COSMO
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Carr GJ;

Trawick JD,

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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential consists their use in the discovery of novel antibiotics, the essential consists themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen correctly for homologous nucleic acids squence represents an essential prokaryotic cellular proliferation protein.

Correctly and prokaryotic cellular proliferation protein.

Correctly from WiPo at the squence directronic format directly from WiPo at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 VVETPSELFKLVDAVVICTPNKFHADLSIEALNHGVHVLCEKPMAMTTEECDRMIEAANK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 KFGVVVVGVGRAGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLEDALSSQE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KLKVGVIGVG--GIAQDRHI------PALLKLKDTVSLVAVQDINTVQMIDVAKRFNIPH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Indels
                                                                                                                                                                                                                                                                                  Ohlsen KL, Zyskind JW, Wall D,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum protein fragment SEQ ID NO: 5808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.9%; Score 119.5; DB Best Local Similarity 27.9%; Pred. No. 0.004; Matches 43; Conservative 21; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 KGKVL----HEEHVELLMEEFAFLKKEVVGKDLL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Seq ID No 12458; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                                2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
                                                                                                                                                              22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
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                                            21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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Yamamoto RT,
                                                                                                                                          27 - NOV - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                             The present invention relates to the genomic sequence of Pyrococcus abyssi (see AARB6431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centifigrade.
Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPWTLSLAAAQELWELAEQKGKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PE-KLKVGIIGCGNIFNLAHKPALKSLRTIAKVVAVMDIDEEAARKAGKELNAKVFTSLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PERKFGVVVVGVGR----AGSVRMRDLRNPHPSSAFLNLIGFVSRRELGSIDGVQQISLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LHEEHVELLMEEFAFLKKEVVGKDLLKGS--LLFTAGPLEEERFGFPA-----FSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LFVGHVR-----RFDKRWIQIKDIIKSRNILPMQIRKIEVQHLPFPADYWYWDESKSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 I-----SRLTWL----VSLFGELSLVSATLEERKEDQYMKMTVCLETEKK--SPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 VIVDLGVHVTDFLRWFFESEPIEVFAVGKAIRGEARVNKTHDHVVMFIKFEGGKTGIGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWIEEKGPGLKRNRYLSFHF - - - - KSGSLE - - - - NVPNVGVNKNIFLKDQNIFVQKLL
                                                                                                                                                              nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                              Lecompte 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.0%; Score 121; DB 22; Length 341; Best Local Similarity 21.9%; Pred. No. 0.0028; Matches 70; Conservative 54; Mismatches 137; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus cellular proliferation protein #1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                            Phierry JC, Prieur D, Dietrich J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                   Claim 7; Pages 1109-1110; 1657pp; French
(IFRE-) IFREMER INST FR RECH EXPL MER
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                                                                                                                                                                                    proteins useful in industry
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                                         Thierry
                                                                                                                 WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AA;
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                                            Forterre P,
Querellou J,
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AAU36865

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(BADI ) BASF AG.
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09 - JUL - 1999

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14 - JUL - 1999
                                                                                                                                                            23-JUN-2000;
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14-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1999
   4
                                                                                                                                                                                                                                                                                                                                                                   sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, unclet acids, vitamins, saccharides and organic acids, in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                   mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LEDALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLVEYPMTLSLAAAQELWELAEQKG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 PDDVLTRDDIDAVLIATPARTHADLVVKAAAAGKHVFVEKPMAVTLEDADRAINAAREAN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 VVVVGVGRAGSVRMRDLRN------PHPSSAFLNLIGFVSRRELGSIDGVQQIS 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; carbon metabolism and energy production;
                                                                                                                                                                                                Hayashi M, Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                          present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 116.5; DB 22; Length 337; 55.1%; Pred. No. 0.0076; ve 24; Mismatches 70; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum SMP protein sequence SEQ ID NO:288
                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO: 5808; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 KVLHEEHVELLMEEFAFLKKEVVGKDLLKGSLL------FTAGP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 TVLQVGFNRRFAAGFAAARARIDAGDIGTPQLLRSVTRDPGPFTADP 161
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                                                                                                                                                                                                           Ozaki A;
                                                                                                                                                                                                 Ando S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB79386 standard; Protein; 337 AA
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                                                                                                                       99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                18-DEC-2000; 2000EP-0127688
                         Corynebacterium glutamicum.
                                                                                                                                                                                                 Mizoguchi H,
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organic acid synthesis
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                                                                                                                                                                                                                                  WPI; 2001-376931/40.
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Matches 42; Conserv
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                                                                                                                                    07-APR-2000;
03-AUG-2000;
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                                                                                                                       16-DEC-1999;
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Tateishi N,
                                                                        20-JUN-2001
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AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebbacterium diphtheriae in a subject. (I), (III) or host cells containing them are used to map genomes of organisms related to
SMP protein, sugar metabolism and oxidative phosphorylation protein, fine chemical production, organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromathc compound; vitamin; cofactor; polyketide; aiogid; diagnosis; Corynebacterium diphtheriae; evolutionary study.
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metabolism and oxidative phosphorylation protein for production or
modulation of production of fine chemicals e.g. amino acids,
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C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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Xu HH;
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N-PSDB; AAS51970.
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Yamamoto RT,
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26-MAY-2000;
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invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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99bts7 homo sapten
09but12 homo sapten
09pou6 homo sapten
043658 homo sapten
09h98 homo sapten
09h99 homo sapten
000532 homo sapten
000532 homo sapten
09ctl3 neurospora
09ks1 homo sapten
09ut34 homo sapten
09ut34 homo sapten
09ut34 arabidopsis
        lycopersico
                                                                                                                                                          024022 lycopersico
098s67 guillardia
                                                                                                                                                                                                                Ogluni plasmid psb
Oglgh4 epiphyas po
                 human immun
                        escherich1a
                                                                                                                                                                          O9brb5 homo sapten
O9u6w5 caenorhabd1
                                homo sapien
                                                                                                                                                                                                  Ognsrl homo sapien
044797 caenorhabdi
                                                                                                                                                                                           drosophila
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
MEDLINE-99397451; PubMed-10470850;
Kaneko T., Katcho T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
"Structures of the regions of 1,011,550 bp covered by seventeen Pl and TAC clones.";
DNA Res. 6:183-195(1999).
EMBL; AB017068; BAB11366.1; -.
EMBL; AB017068; BAB11366.1; -.
"TOTAL CRC64;
                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                099553
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MUTATOR-LIKE TRANSPOSASE-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 10;
Pred. No. 0.95;
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       Q9S738
Q9Q553
P75909
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Q9KSC1
Q9UK53
Q9UIJ4
                                                                                                                                   09VJ28
09C8V1
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098S67
09BRB5
09U6W5
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Q91GH4
                                             0901J2
09P0U6
043658
09HD98
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000532
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09NSR1
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Best Local Similarity luv...
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KKRIMHC 569
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NCBI_TaxID=3702;
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                                                             (without alignments) 952.238 Million cell updates/sec
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                                                    1, 2002, 14:43:08 ; Search time 1.2717 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                          562222 segs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q9BRW8
Q96QL4
Q9DD21
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Q9LML0
Q9D6S2
Q9QXV3
Q9M149
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Q03949
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Q9ST63
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O49511
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_invertebrate:*
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 200000000
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sp_mhc:*
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1 KKRIMHC
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A Arakawa T., Hara A., Fibata K., Yoshino M., Itch M., Ishii Y.,
A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori P., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rubell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrim L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
A Baka J., Boffelli D., Bojinga N., Carninci P., de Bonaldo M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Florence C., Fujita M., Mombaerts P.,
Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                                     SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K., Schueller C.,
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MUDR TRANSPOSABLE ELEMENT - LIKE PROTEIN (MUDR TRANSPOSABLE ELEMENT-
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 633;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL021710; CAA16721.1; -..
EMBL; AL161548; CAB78843.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR004332; MuDR.
Pfam; PF03108; MuDR; 1.
SEQUENCE 633 AA; 72930 MW; 3FC298BF2218C623 CRC64;
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Last annotation update)
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Pred. No. 0.99;
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STRAIN-C57BL/6J; TISSUE-EMBRYONIC LIVER;
MEDLINE-21085660; PubMed-11217851;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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2500001N03RIK.
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| 591 KKRIMHC 597
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                                                                LIKE PROTEIN).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.",
Nature 409:685-690(2001).
EMBL; AK010847; BAB27219.1; -.
MGD; MGI:1917355, 2500001N03Rik.
TherPro: PPRO0683; GPO_LDH_MOCA.
Pfam; PF01408; GFO_LDH_MOCA.
SEQUENCE 295 AA; 33324 MW; F2E1682BD77032A4 CRC64;
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.
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                                                                                                                                                                                                                                   Length 295;
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                                                                                                                                                                                                                                                                               Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005902; AAH05902.1; ..
InterPro: IPRO06813 GFO_IDH_MOCA.
Pfam: PF01408; GFO_IDH_MOCA.
SEQUENCE 296 AA; 33432 MW; A389AFDDB6ADBABF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:14706).
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2.2;
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Pred. No.
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Matches 6; Conserv
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274 KKRILHC 280
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275 KKRILHC 281
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09D6S2;
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Subject From N. 1.

Medile Sinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., Ashburner M., Stabli F., Yomita M., Wagner L., Washio T., Ashaif K., Okido T., Furuno M., Anno H., Batdarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ashaif M.J., Bult C., Pletcher C., Fullita M., Gariboldi M., Anorshionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Avaribola M., Lee N. R., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshaw Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Anasahi, V., V., Wanshi, V., Kawashi, V.
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NCBL_TaxID=5659;
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mbox{H\"{a}yashizak1}~Y..; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.7%; Score 38; DB 11; Length 303; 85.7%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 AA; 34491 MW; 52D8A3B02EE956EB CRC64;
                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                   303 AA
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                                                                                                                                                                     Created)
                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 403-205 (2016) EMBL; AK002231; BAB21950.1; -- MGD; MCI:1915580; 0610006811Rik. InterPro; IPR000683; GFO_IDH_MOCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01408; GFO_IDH_MocA; 1.
                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 0610006AllRIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, RIBOSOMAL PROTEIN L44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                          275 KKRILHC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111:11
274 KKRILHC 280
            1 KKRIMHC 7
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Q9XZM5
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu S.X., Chan A., Yu G., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H., Toriumi M., Chung M., Goldsmith A., Liu A., Liu A., Luu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A., "Ime Sequence of BAC Floil from Arabidopsis thallana chromosome 1."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                       90.2%; Score 37; DB 5; Length 106; 71.4%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
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FAD; Flavoprotein; Oxidoreductase.
SEQUENCE 512 AA; 56857 MW; 1F63AFA9A1A2C13B CRC64;
                                                                                                                                                                                                                                                        106 AA; 12283 MW; F30A3AB2047B0334 CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2'-5' OLIGOADENYLATE SYNTHETASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 AA.
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                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001327; FAD_pyr_redox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: FAD (BY SIMILARITY).
EMBL; AC067971; AAF82202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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F10K1.11.
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6 KKKVMHC 12
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AT4G01190.
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STRAIN=129/SVJ; TISSUE=BRAIN. EMBRYONIC FIBROBLAST, AND SPLEEN;
MEDLINE=20011419; Pubmed=10542254;
Zeremski M., Hill J.E., Kwek S.S.S., Grigorian I.A., Gurova K.V.,
Garkavtsev I.V., Diatchenko L., Koonin E.V., Gudkov A.V.;
"Structure and regulation of the mouse ingl gene. Three alternative transcripts encode two PHD finger proteins that have opposite effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rancourt D., Garkavtsev I.; "Structural organization and expression pattern of the murine ING1 "Structural organization" ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                 'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 11; Length 508;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58767 MW; 9552B4540CC801A0 CRC64;
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NAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00833; 25A_SYNTH_2; UNKNOWN_1.
PROSITE; PS50152; 25A_SYNTH_3; 1.
PS00SITE; PS50053; UBIQUITIN_2; 1.
SEQUENCE 508 AA; 58767 WW; 9552B4540C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on p53 function.";
J. Biol. Chem. 274:32172-32181(1999).
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                                                                                                                                                                                                                                                                                                                                        EMBL, AK010034, BAB26655.1; --
MGD; MGT:1344390; Oasl.
InterPro; IPR00177; 25A_synth.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR000626; Ubiquitin.
                                     STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000626; Ubiquiti
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00213; UBQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KKRIMHC 7
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: IN THE ADULT, WIDELY EXPRESSED WITH HIGHEST LEVELS IN THYMUS AND TESTIS. EXPRESSED TROUGHOUT THE WHOLE EMBRYO AT ALL STAGES OF DEVELOPMENT EXAMINED. AT DAY 10, HIGHEST EXPRESSION IS FOUND IN THE YOLK SAC WHILE AT DAY 16 AND 18, HIGHER LEVELS ARE FOUND IN THE WEBRYO, HIGHEST EXPRESSION OF ISOFORM -1. DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OF ISOFORM 2 IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
eurosids II; Brassicales: Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL161491; CAB80928.1;
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DOMAIN 210 259 PHD-FINGER.

VARSPLC 1 94 MISSING IN ISOFORM 2).

CONFLICT 203 203 L -> F (IN REF 2).

SEQUENCE 279 AA; 32109 MW; 6765C984EEF179F4 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOUND AT DAY 7.

-1- SIMILARITY: CONTAINS 1 PHD-FINGER DOMAIN.
EMBL, AF177755, AAF16908.1;
EMBL, AF177755; AAF16909.1;
EMBL, AF177757, AAF16910.1;
EMBL, AF177757, AAF16910.1;
EMBL, AF177757, AAF16910.1;
EMBL, AF17757, AAF16910.1;
EMBL, AF17757, AAF169183.1;
EMBL, AF17757, AAF169183.1;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUTATIVE PHOSPHATIDYLINOSITOL KINASE
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                                                     SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=BREAST TUMOR;
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1°,
A; Conservative
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InterPro; IPR001965; PHD.
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67 KRRVLHC 73
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PRT;
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     SEQUENCE FROM N.A.
MEDLINE=91358370; PubMed=1653219;
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Best Local Similarity
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     171 KKRLKHC 177
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21 RKRLLHC 27
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                                                                                                                                                                                                                                                                                                                                                                     1 KKRIMHC 7
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01-JUL-1997 (TrEMBLE). 04, Last sequence update)
01-DEC-2001 (TrEMBLE). 19, Last annotation update)
01-DEC-2001 (Mouse-ear cress).
01-JUL-1997 (Mouse-ear cress).
01-JUL-1997 (Mouse-ear cress).
02-JUL-1997 (Mouse-ear cress).
03-JUL-1997 (Mouse-ear cress).
03-JUL-1997 (Mouse-ear cress).
03-JUL-1997 (Mouse-ear cress).
04-JUL-1997 (Mouse-ear cress).
04-JUL-1997 (Mouse-ear cress).
05-JUL-1997 (Mouse-ear cress).
05-JUL-1997 (Mouse-ear cress).
06-JUL-1997 (Mouse-ear cress).
06-JUL-1997 (Mouse-ear cress).
07-JUL-1997 (Mouse-ear cress).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INSERTION ELEMENT IS895 HYPOTHETICAL 21.9 KDA PROTEIN (ORFI).
                                                                                                                                             Score 34; DB 10; Length 401;
Pred. No. 21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 10; Length 431;
Pred. No. 22;
0; Mismatches 1; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Scheet P., Maggil L.;
"The sequence of A. thaliana IG002N01.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Waterston R.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF007269; AAB61030.1; -.
InterPro; IPR002499; PPPSK.
Pfam: PF01504; PPPSK.
Pfam: PF01504, PPPSK; 1.
SMART; SM00330; PIPKc; 1.
SEQUENCE 431 AA; 49356 MW; 07A53F23BDDD942B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wash U;
"The A. thaliana Genome Sequencing Project.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                8A12D10DA2DED4CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                SEQUENCE 401 AA; 45659 MW;
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nilarity 85.7%;
Conservative (
                                                                                                                                             82.9%;
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04,
19,
InterPro; IPR002498; PIP5K.
                    Pfam; PF01504; PIP5K; 1. SMART; SM00330; PIPKc; 1.
                                                                                                                                        Query Match 82.9
Best Local Similarity 85.7
Matches 6; Conservative
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STRAIN-CV COLUMBIA;
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 KKRIEHC 389
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Q03949;
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004613;
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004613
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Gaps
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Solanum tuberosum (Potato).
Sperartophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ZOBELL ATCC14405;
MEDLINE-21101859; PubMed=11160097;
HeikKilae M.P., Honisch U., Wunsch P., Zumft W.G.;
"Role of the Tat transport system in nitrous oxide reductase translocation and cytochrome cdl biosyntheis in Pseudomonas stutzeri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                       Length 189;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE INTERNAL ROTENONE-INSENSITIVE NADH DEHYDROGENASE.
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 183:1663-1671(2001).

EMBL, AJ299712; CAC29149.1; -
InterPro; IPR002033; UPP0032.

Pfam; PF0002: UPP0032; 1.

PROSITE; PS01218; UPPF0032; 1.

SEQUENCE 267 AA; 29439 MW; 4369EB5E38BCD736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                       80.5%; Score 33; DB 2; ilarity 71.4%; Pred. No. 17; Conservative 1; Mismatches
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RC STRAIN=CV. DESIREE; TISSUE=LEAF;
RA MEDLINE=20040052; PubMed=10571867;
RA RESMUSSON A.G., Svensson A.G., Ronop V., Grohmann L., Brennicke A.;
RT "Homologues of yeast and bacterial rotenone-insensitive NADH
RT mitochondria.";
RT mitochondria.";
RT mitochondria.";
RT mitochondria.";
RT mitochondria.
RM FAD; FAD_DY_Tredox.
DR Pfam; PF00070; pyr_redox; l..
RW FAD; Flavoprotein; NAD; Oxidoreductase.
SQ SEQUENCE 495 AA; 54902 MW; GAFF0807BEB01340 CRC64;
RATCHONGRIA.
RATCHOR SAA; S4902 MW; GAFF0807BEB01340 CRC64;
RATCHOR SAA; S4902 MW; GAFF0807BEB01340 CRC64;
RATCHOR SAA; S4902 MW; Mismatches 0; Indels 0; Gaps 0;
RATCHOR SEARCHAG 230
SSaarch completed: November 1, 2002, 14:49:46
Job time: 3.2717 secs
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us-09-606-129a-18.rsp

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 1, 2002, 14:41:32 ; Search time 0.360129 Seconds (without alignments) 752.611 Million cell updates/sec Run on:

US-09-606-129A-18 41 1 KKRIMHC 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	rattus no	homo sapien	mus musculu	saccharomyc	mus musculu		esche	homo sapien		solanum tub						_		meth	mus musculu	ther		saccharomyc	_	_		saccharomyc	schizosacch	homo sapien	haemophilus	haemophilus	caenorhabdi	Н.	emericella
	rig		04	£2	20	78	85	79	30	12	27	43	41	47	88	18	<u>۷</u>	68	71	13	i.6	19	90	26	37	32	23	64	81	41	04	41	20	21
	esc	468	P53004	09z2f2	P40020	P45878	P26885	P37179	926	107	314	178	103	519	447	136	931	P52468	602	973	9x1	571	388	553	030	484	P3422	010264	437	057341	448	3	24120	786
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SUMMARIES	DI	BIEA_RAT	BIEA_HUMAN	OASL_MOUSE	PIP1_YEAST	FKB2_MOUSE	FKB2_HUMAN	HYBA_ECOLI	DYR2_HUMAN	AMP1_LYCES	AMPL_SOLTU	RL44_TRYBB	Y091_NPVOP	CYCH_XENLA	SUN_HAEIN	CUL3_HUMAN	CUL3_MOUSE	UL52_HSV7J	YZ09_METJA	PRKD_MOUSE	RL36_THEMA	SECB_BUCAI	YHP5_YEAST	YZG1_CAEEL	RANT_BPP22	ODPB_RAT	SHP1_YEAST	YD2H_SCHPO	DYR3_HUMAN	AFUB_HAEIN	REP_HAEIN	YK62_CAEEL	APU_	SEPA_EMENI
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æ	Query	100	92	85	80	78	78	78	78	78	78	75	75	75	75	75	75	75	73	73	70	70	70	70	70	70	2	70	70	70	70	70	70	70
	Score	41	38	35	33	32	32	32	32	32	32	31	31	31	31	31.	31		. 30	30	29	29	58	29	29	29	29	29	29	29	29	29	29	29
	Result No.	1	7	3	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

34 23 35 25 36 37 37 37 37 37 37 37 37 37 37 37 37 37	28 68.3 113 28 68.3 249 28 68.3 314 28 68.3 334 28 68.3 335 28 68.3 428 28 68.3 459 28 68.3 447 28 68.3 447 28 68.3 447		FLIT_BACSU IPYE_RICPR YOAM_BACSU IDSA_METTM ULIG_HSVGU GBA1_DICDI DGTP_MYCSM NEK3_HUMAN NEK3_HUMAN NEK3_HUMAN NEK3_HUMAN NEK3_LUMAN	P39740 bacillus su Q92cw5 rickettsia P05449 rhodopsaudo P45910 bacillus su Q54479 methanobact P24442 human herpe P16894 dictyostell O52199 mycobacteri P51956 homo saplen P98119 desmodus ro P15538 desmodus ro P2555 escherichia
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BEESULT 1 BIES AAC 01-19 BIES AAC 01-19 BIES AAC 01-19 BIES OC 01-19 BIE
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                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=9314333; pubMed=8424666;
Maincs M.D., Trakshel G.M.;
"Purification and characterization of human biliverdin reductase.";
Arch. Biochem. Biophys. 300:320-326(1993).
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                       Maines M.D., Polevoda B.V., Huang T.-J., McCoubrey W.K. Jr.; "Human biliverdin IXalpha reductase is a zinc-metalloprotein.
Characterization of purified and Escherichia coli expressed
                                                                                                      100.0%; Score 41; DB 1; Length 295; 100.0%; Pred. No. 0.15; tive 0; Mismatches 0; Indels
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
C->A: LOSS OF ACTIVITY.
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
W; 219C8EA96C150588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Komuro A., Tobe T., Nakano Y., Yamaguchi T., Tomita M.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordes M., Wollam C., Carter T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                    296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 3-36; 48-74 AND 228-248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 235:372-381(1996).
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=96202961; PubMed=8631357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE-95014177; Pubmed=7929092;
                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
                                                                                33565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-117 FROM N.A.
                                                                                                                                Conservative
                                                                                                                                                                                                                                    STANDARD;
             280
291
292
73
73
280
291
                                                                                                                                                                                                                                                                                                                 BLVRA OR BLVR OR BVR.
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
 279
280
291
292
73
280
291
295 AA;
                                                                                                                Local Similarity
ses ·7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 3-22.
                                                                                                                                                                           274 KKRIMHC 280
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                     1 KKRIMHC 7
                                                                                                                                                                                                                                  BIEA_HUMAN
P53004;
                                                                                                                                                                                                                                                                                                        reductase).
                                                                      MUTAGEN
SEQUENCE
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymes.
                                                MUTAGEN
                                                            MUTAGEN
                        METAL
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                                     METAL
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Tiefenthaler M., Marksteiner R., Neyer S., Koch F., Hofer S.,

Tiefenthaler M., Marksteiner R., Neyer S., Koch F., Hofer S.,

Tiefenthaler M., Schneider R., Heufler C.;

"M1204, a novel 2',5' oligoadenylate synthetase with a ubiquitin-like extension, is induced during maturation of murine dendritic cells.";

J. Immunol. 163:760-766(1999).

L. J. Immunol. 163:760-766(1999).

L. J. Timunol. MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.

L. CATALYTIC ACTIVITY: BINDS DOUBLE-STRANDED RNAS.

THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAS.

THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAS.

THE HOPPERST IS STRONGLY EXPRESSED IN SPLEEN DRUDRITIC CELLS, THE AMOUNT INTERACES DURING THE MATROW-DERIVED DENDRITIC CELLS, THE AMOUNT OF THE HIGHEST LEVELS BEING IN THYMUS, LUNG, AND BONE MARROW.

THE HIGHEST LEVELS BEING IN THYMUS, LUNG, AND BONE MARROW.

THE HIGHEST LEVELS BEING IN THYMUS, LUNG, AND BONE MARROW.

L. SIMILARITY: CONTAINS I UBIGUITIN-LIKE DOMAIN.

L. SIMILARITY: CONTAINS I UBIGUITIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
54 kpa 2'-5'-0ligoadenylate synthetase like protein (EC 2.7.7.-) (p54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                                                 ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
A -> T (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.62;
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                                                                                                                                                                                                                                        SIMILARITY: TO E.COLI YHHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33488 MW;
                                                                                                                                                                    EMBL; X93086; CAA63635.1; -. EMBL; U34877; AAC35588.1; -. EMBL; AC005189; AAC25526.1; -. MIM; 109750; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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275 KKRILHC 281
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CONFLICT
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CONFLICT
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OASL_MOUSE
                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
WEDLINE-97339480; PubMed-9196079;
RUSSDAR K., Percelra S., Platt T.;
"RNA binding analysis of yeast REF2 and its two-hybrid interaction with a new gene product, FIRI.";
Gene Expr. 6:241-258(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Polymerase-interacting protein 1 (Factor interacting with REF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.4%; Score 35; DB 1; Length 473; llarity 71.4%; Pred. No. 4.2; Conservative 2; Mismatches 0; Indels
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UBIQUITIN-LIKE.
570E0E08A51C8460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA-binding; Transferase; Nucleotidyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   925 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGNIC PROCESS OF STANDARY PROSTITE: PSO0812: 25A_SYNTH_1; FALSE_NEG. PROSTITE: PSO0832: 25A_SYNTH_2; 1.
PROSTITE: PSS0152: 25A_SYNTH_2; 1.
PROSTITE: PSS0152: 25A_SYNTH_3: 1.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001201; PAP_25A_core.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR000626; Ubiquitin.
                                                                                                                                                                                                                                                                                                     EMBL; AF068835; AAD02818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 AA; 54625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIP1 OR FIR1 OR YER032W.
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hes 5; Conserv
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P40020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SEQUENCE FROM N.A.

STRAIN-129/SVJ; TISSUB-Liver;

RA Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,

RA Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,

RA Burakoff S.J., Dilella A.G.;

RY "Structural organization of the genes encoding human and murine rext of genes of the genes encoding human and murine as a component of membrane cytoskeletal scaffols.

- FUNCTION: PPISASS accelerate the folding of proteins. May function as a component of membrane cytoskeletal scaffols.

- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC CHARYMER REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.

- SUBUNIT: Interacts with the C-terminal domain of 4.1G.

- SUBUNIT: Interacts with the C-terminal domain of 4.1G.

- SUBCATEON (PROBABLE).

- SUBCATEON (PROBABLE).
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                                                                                                                                                                                                                                                       Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREVENT SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                           80.5%; Score 33; DB 1; Length 925; 71.4%; Pred. No. 22; 1: Mismatches 1; Indels
                                                                                                                                                        663 663 R -> P (IN REF. 2).
925 AA; 104701 MW; 707D9839EE31322B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00453. FKBP_PPIASE_1: 1.
PROSITE: PS00454: FKBP_PPIASE_2: 1.
PROSITE: PS00599: FKBP_PPIASE_3: 1.
Isomerase: Rotamase: Signal: Endoplasmic reticulum.
SIGNAL
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InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
                                                                                            EMBL; U17262; AAB46625.1; -.
EMBL; U18778; AAB64565.1; -.
SGD; SO000834; FIR1.
CONFLICT 663 663
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                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                     3est Local Similarity
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                                                                                                                                                                                                                                                                                                                                  841 KKRLSHC 847
                                                                                                                                                                                                                                                                                           1 KKRIMHC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FKB2_MOUSE
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                 Query Match
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CHAIN
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FKB2_MOUSE
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FTIG-VAR_006410.

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SEQUENCE FROM N.A.
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                                                                                                                                          1 KKRIMHC 7
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                                                                                                                                                                                                           HYBA_ECOLI
P37179:
                                                         SEQUENCE
             VARIANT
                                  VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                              Gaps
                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93112052; PubMed-1281998; Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.; "Chromosomal band assignments of the genes encoding human FKBP12 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREVENT SECRETION FROM ER (POTENTIAL) S -> TA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 189:819-823(1992).
-1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00453; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_1; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
                                             0;
                                                                                                                                                                                                                                                                                                               TISSUE-Colon carcinoma;
MEDILNB-91319747; PubMed-1713687;
Jin Y.-J., Albers M.W., Lane W.S., Bierer B.E., Schreiber S.L.,
Burakoff S.J.;
                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of a membrane-associated human FK506- and rapamycin-binding protein, FKBP-13.";
Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991).
                      Length 140;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED (PROBABLE).
-!- TISSUE SPECIFICITY: T-CELLS AND THYMUS.
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
15344 MW; F4E7FCC7766A0416 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FK506-BINDING PROTEIN.
                      DB 1;
                                5.4;
                                                                                                                                                  141 AA
                                             Mismatches
                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
                      78.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M65128; AAA58473.1; -. EMBL; M75099; AAA36563.1; -. PIR; JC1365; JC1365.
                                             Conservative
                                                                                                                                                  STANDARD;
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141
21
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MIM; 186946; -
                    Query Match
Best Local Similarity
140 AA;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                 111: 11
34 KKRVDHC 40
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138
21
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                                                                   1 KKRIMHC 7
                                                                                                                                                FKB2_HUMAN P26885;
SEQUENCE
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VARIANT
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli ol15:HT and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                           Gaps
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STRAIN-KIZ. 7 MG165;
MEDLINE-9742617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-0157.HT / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
Medlevett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Menon N.K., Chatelus C.Y., Dervartanian M., Wendt J.C., Shammugam K.T., Peck H.D. Jr., Przybyla A.E.; "Cloning, sequencing, and mutational analysis of the hyb operon encoding Escherichia coli hydrogenase 2."; Bacteriol. 176:4416-4423(1994).
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                   Score 32; DB 1; Length 141; Pred. No. 5.4;
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                                                                                                                                                                                                                                                    1; Indels
                                                                                                                            9F4751CA7D82D064 CRC64;
                          /FTId=VAR_006411
                                                                                        /FTId=VAR_006412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrogenase-2 operon protein hybA precursor.
HYBA OR B2956 OR Z4350 OR ECS3881.
Escherichia coli, and
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 AA
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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                                                                                                                            15654 MW;
                                                                                                                                                                                      78.0%;
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                                                                                                                            141 AA;
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Best Local Similarity
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Query Match
Best Local Similarity
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SEQUENCE
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
ACTIVITY OF HYDROGENASE 2 DURING ITS CATALYTIC TURNOVER.
COFACTOR: BINDS 3 4FE-4S CLUSTERS AND A 3FE-4S CLUSTER.
SUBCELLULAR LOCATION: PETIPLASMIC.
SIMILARITY: THE IRON-SULFUR EDRINGS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE THE SMALL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                   IRON-SULEUR I (4FE-4S) (POTENTIAL).
IRON-SULEUR I (4FE-4S) (POTENTIAL).
IRON-SULEUR I (4FE-4S) (POTENTIAL).
IRON-SULEUR I (4FE-4S) (POTENTIAL).
IRON-SULEUR 2 (3FE-4S) (POTENTIAL).
IRON-SULEUR 2 (3FE-4S) (POTENTIAL).
IRON-SULEUR 2 (3FE-4S) (POTENTIAL).
IRON-SULEUR 3 (4FE-4S) (POTENTIAL).
IRON-SULEUR 4 (4FE-4S) (POTENTIAL).
                                                                                                                                                                                           EMBL; U09177; AAA21589.1; --
EMBL; U28377; AAA69165.1; --
EMBL; AE000382; AAC76032.1; --
EMBL; AE000552; AAC76032.1; --
EMBL; AP002563; BAB37304.1; --
ENSP; P55907; INTR.
ECGEnne; EC11799; hybA.
InterPro; IPR001450; 4Fe45_ferredoxin.
PROSTTE; P500198; 4Fe45_FERREDOXIN; 1.
PROSTTE; P500198; 4Fe45_FERREDOXIN; 1.
Oxidoreductase; Signal; Periplasmic; Iron-sulfur; 4Fe-45; 3Fe-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                           HYDROGENASE-2 OPERON PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 328;
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                         OF HYDROGENASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA;
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Best Local Similarity
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SIGNAL 1
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                                                           -!- CAUTION:
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Q92630;
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SEQUENCE
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InterPro: IPR002290; Ser_thr_pkinase.
Pfam; PP00069; pkinase; 2.
SMART; SM00220; S_TRC: 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
Transferase; Serine-threonine-protein kinase; ATP-binding; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                             Becker W., Joost H.-G.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IN VITRO; CAN PHOSPHORYLATE HISTONES H3 AND H2B ON SER
AND THR RESIDUES. MAY BE INVOLVED IN THE REGULATION OF CELLULAR GROWTH AND/OR DEVELOPMENT.
                                                                                                "Sequence characteristics, subcellular localization, and substrate specificity of DYRK related kinases, a novel family of dual specificity protein kinases.";
J. Biol. Chem. 273:25893-25902(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- FTM: AUTHOPHOSPHORYLATED ON TYR RESIDUES.
-:- SIMILARITY: BELOGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MNB/DYRK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
      Becker W., Weber Y., Wetzel K., Eirmbter K., Tejedor F.J., Joost H.-G.;
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Pred. No. 20;
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NCBI_TaxID-4081;
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AF2C6822ED9522D7 CRC64;
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ATP (BY SIMILARITY).
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MEDLINE=98421512; PubMed=9748265;
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y13493; CAA73885.1; -. EMBL; Y09216; CAA70418.1; -. HSSP; Q16539; IWFC. MIM; 603496; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
178
178
275
528 AA;
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|||:|| KRIVHC 53

48

qq

RESULT 10

KRIMHC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Teucoline aminopeptidase: an inducible component of the defense response in Lycopersicon esculentum (tomato).";
Proc. Natl. Acad. Sci. U.S.A. 90:9906-9910(1993).

- Proc. Natl. Acad. Sci. U.S.A. 90:906-9910(1993).

- FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR TORNOVER OF INTRACELLULAR PROTEINS.

- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-i-Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.

- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).

- INDUCTION: BY WOUNDING.

- INDUCTION: BY WOUNDING.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI7; ALSO KNOWN AS THE CYTOSOL AMINOPEPTIDASE FAMILY.
                   SEQUENCE FROM N.A.
STRAIN-CV. PETO 238R; TISSUE-Leaf;
MEDLINE-96421572; Pubmed-8824220;
GU Y.Q., Chao W.S., Walling L.L.;
"Localization and post-translational processing of the wound-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000819; Peptidase_M17.
Pfam; PF00083; Peptidase_M17.1.
Pfam; PF00083; Peptidase_M17.N:1.
PRINTS; PR00481; LAMNOPPTDASE.
PROSTTE; PS00631; CYTOSOL_AP; 1.
Transit peptide; Chloroplast; Aminopeptidase; Hydrolase; Zinc. TRANSIT 1.
54 571 AMINOPEPTIDASE 1.
                                                                                                                                                                                                                                                                                                                        Milligan S.B., Gasser C.S.; "Nature and regulation of pistil-expressed genes in tomato."; Plant Mol. Biol. 28:691-711(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> L (IN CLONE PBLAP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. PETO 238R; TISSUE-Leaf;
MEDLINE-94052201; PubMed-8234334;
Pautot V., Holzer F.M., Reisch B., Walling L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N (IN REF. 2).
S (IN REF. 3).
                                                                                                                                                            leucine aminopeptidase proteins of tomato.";
J. Biol. Chem. 271:25880-25887(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32;
                                                                                                                                                                                                                                                                      STRAIN~CV. VF36; TISSUE-Pistil;
MEDLINE=95375233; PubMed=7647301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^-
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 103-571 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U50151; AAC49456.1; -. EMBL; U50152; AAC49457.1; -. EMBL; U20593; AAR80498.1; -. HSSP; P00727; 1LAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%;
83.3%;
                                                                                                                                                                                                                                             SEQUENCE OF 49-571 FROM N.A.
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Best Local Similarity
''^a 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271
315
515
571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M17.002;
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169
342
347
427
429
354
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ACT_SITE
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VARIANT
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RRYKY RYKY RRYKY R
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"General roles of abscisic and jasmonic acids in gene activation as a result of mechanical wounding.";

"General roles of abscisic and jasmonic acids in gene activation as a result of mechanical wounding.";

"In Plant Cell 4:1157-1170(1992).

"In CATALYTIC ACTIVITY: Release of an N-terminal amino acid; Xaa-j-catalytic Activity is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.

"COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).

"Including Pro although not Arg or Lys, and Xbb may be Pro.

"COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).

"Insurance of the complex of the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Aminopeptidase, chloroplast precursor (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (LAP) (Leucyl aminopeptidase)
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. DESIREE;
MEDLINE-9433796; PubMed-7765119;
HENDERS K., Prat. S., Willmitzer L.;
"Functional analysis of a leucine aminopeptidase from Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV DESIREE; TISSUE-Leaf;
MEDLINE=9306746; PubMed=1392612;
Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
Willmitzer L., Prat S.;
                           573 AA
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000819; Peptidase_M17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00883; Peptidase_MI7; I.
Pfam; PF02789; Peptidase_MI7.N: 1.
PRINTS: PR00481; LAMNOPPTDASE.
PROSITE; PS00631; CYTOSOL_AP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOSOL AMINOPEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X77015; CAA54314.1; -.
EMBL; X67845; CAA48038.1; -.
PIR; S24769; S24769.
PIR; PQ0470; PQ0470.
HSSP; P00727; 1LAM.
MEROPS; M17.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 19-573 FROM N.A.
                                                                                                                                                                                                                                                                                             Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Planta 194:230-240(1994).
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4113;
                     AMPL_SOLTU
P31427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WOUNDING
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AMPL_SOLTU
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Mismatches

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Query Match

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-OCCYTE;
MEDLINE-95645408; PubMed-7957080;
Labbe J.-C., Martinez A.-M., Fesquet D., Capony J.-P., Darbon J.-M.,
Labbe J.-C., Martinez A.-M., Morin N., Cavadore J.-C., Doree M.;
Labbe J.-C., Martinez A.-M., Morin N., Cavadore J.-C., Doree M.;
The Monols associates with a p36 subunit and requires both nuclear translocation and Th176 phosphorylation to generate cdk-activating kinase activity in Kanopus occytes.";
EMBO J. 13:5155-5164(1994).

-!-FUNCTION: Requireds CDK7, the catalytic subunit of the CDK-activating kinase (CAK) enzymatic complex. CAK activates the cyclin-associated kinases CDC2/CDK1, CDK2, CDK4 and CDK6 by
                                                                                                                                                                                                                                                                                                     "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 29.3 kba protein (ORF92).
Orgyia pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
                                                                                                                                                                                                                                              MEDLINE-97271300; Pubmed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrman G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.6%; Score 31; DB 1; Length 279; 66.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .l protein.
279 AA; 29289 MW; 6FA4DAA01009DBF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1996 (Rel. 34, Created)
10-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2001 (Rel. 40, Last annotation update)
Cyclin H (Mol5-associated protein) (p36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA
                     279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U75930; AAC59091.1; -.
                                                                                                                                                                                                                                                                                                                        polyhedrosis virus genome.
Virology 229:381-399(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :1:111
233 QRVMHC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KRIMHC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martinez A.-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYCH_XENLA
P51947;
                   Y091_NPVOP
010341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
CYCH_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                                                                                                                                                   Gaps
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   Aminopeptidase; Hydrolase; Zinc.
                                                                                                             2 (BY SIMILARITY).
1 (BY.SIMILARITY).
1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                            Score 32; DB 1; Length 573;
Pred. No. 22;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 1; Length 105; Pred. No. 6.5; 1; Indels 1; Indels
                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                           3152145A4A7FB291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FA19423F109E7819 CRC64;
                 CHLOROPLAST (POTENTIAL).
AMINOPEPTIDASE.
                                                                      ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
60S ribosomal protein L44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                         POTENTIAL
                                                          POLY - ALA.
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InterPro; IPR000552; Ribosomal_L44E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002841; Ribosomal_L44E; 1.
PROSITE; PS01172; RIBOSOMAL_L44E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-EATRO 1125;
MEDLINE-90251460; Pubmed-2339065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.

INIT_MET 0 0 B
SEQUENCE 105 AA; 12322 MW;
peptide; Chloroplast;
                                                                                                                                                                                                           60122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00935; Ribosomal_L44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.68;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52122; CAA36367.1; -.
                                                                                                                                                                                                                                                78.08;
                                                                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prypanosoma brucei brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.6
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                     54
169
342
347
367
427
429
354
431
573 AA;
                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          111:11
48 KRIVHC 53
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                                                                                                                                                                  ACT_SITE
ACT_SITE
SEQUENCE
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RESULT 12

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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
threconine phosphorylation. CAK complexed to the core-TFIIH basal transcription factor activates RNA polymerase II by serine phosphorylation of the repetitive carboxyl-terminus domain (CTD) of its large subunit (POLR2A), allowing its escape from the promoter and elongation of the transcripts. Involved in cell cycle control and in RNA transcription by RNA polymerase II. Its expression and activity are constant throughout the cell cycle (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95350630; PubMed=7542800; Richard K Walle Statemen R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Reilavege A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm. C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE SUN (BACTERIAL) / NUCLEOLAR PROTEIN
                                                                                                                                                SUBGNIT: Associates primarily with CDK7 and MAT1 to form the CAK complex. CAK can further associate with the core-TFIIH to form the TFIIH basal transcription factor.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00292; CYCLINS; FALSE_NEG.
Transcription regulation; Cell cycle; Nuclear protein; Cyclin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 266 R -> Y (IN REF. 2; AA SEQUENCE).
323 AA; 37600 MW; 14BCDCA000843DC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P51946; LJKW.
INTERPRO, INTERNO053; Cyclin.
Pfem: PRO0134; cyclin; L.
SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U20505; AAA62236.1; -.
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Best Local Similarity 71.4.
5; Conservative
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                                                                                                                                   similarity).
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274 KKRLDHC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KKRIMHC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUN_HAEIN
P44788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NOL1/NOP2 (EUKARYOTES) FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE=98406061; PubMed=9733711;
Du M., Sansores-Garcia L., Zu Z., Wu K.K.;
"Cloning and expression analysis of a novel salicylate suppressible gene, Hs-CUL-3, a member of cullin/Cdc53 family.";
J. Biol. Chem. 273:24289-24292(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michel J.J., Xiong Y.;
"Human CDL-1, but not other cullin family members, selectively interacts with SKP1 to form a complex with SKP2 and cyclin A." Cell Growth Differ. 9:435-449(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1; Length 451;
Pred. No. 28;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                    451 AA; 50597 MW; D91FAB88FFDE34B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CULL3_HUMAN STANDARD; PRT; 768 AA. Q13618; 075415; Q9UBI8; Q9UE77; 01-NOY-1997 (Rel. 35, Created) 16-NOY-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cullin homolog 3 (CUL-3).
                                                                                                                                                                                                          InterPro; IPR001678; Noll_Nop2_Sun.
InterPro; IPR000139; NusB.
InterPro; IPR000051; SAM_bind.
Pfam; PF01189; Noll_Nop2_Sun; 1.
Pfam; PF01029; NusB; 1.
                                                                                                                                                                                                                                                                                                        ProDom; PD005242; NusB; 1.
PROSITE; PS01153; NOL1_NOP2_SUN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Colon carcinoma;
MEDLINE=98326596; PubMed=9663463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                              EMBL; U32745; AAC22284.1; -. TIGR; HI0624; -.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUL3 OR KIAA0617.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
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88 KTRIVHC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKRIMHC 7
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRSRS (IN REF. 3).
DVFERYYRGHARRLITUKSVSDDSE -> MYLNVIINNTW
QGPGQURVFLMTK (IN REF. 5).
AlAOZ022480BF099 CRG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHLRQTLLDMIARERKGEVVD -> GSSTANSIGYDCKRAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    As Score 31; DB 1; Length 768; Similarity 66.7%; Pred. No. 47; 4; Conservative 2; Mismatches 0; Indels
                                                                           Yu W., Sarginson J., Gibbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        D -> G (IN REF. 3).
                                                                                                                                                                                                                                                                      EMBL, AF064087, AAC36304.1; --
EMBL, AB011517, BAA31592.1; --
EMBL, AF062537, AAC36682.1; --
EMBL, U58089; AAC50546.1; --
EMBL, AF052447, AAC28621.1; --
MIM; 603136, --
                                                                                                                                                                                                                                                                                                                                                                 min, December 1 PR001373; Cullin. Pfam; PF00888; Cullin; 1. SMART; SM00182; CULLIN; 1. PROSITE; PS01256; CULLIN, 1. PROSITE; PS50069; CULLIN, 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     768 AA; 88930 MW;
                                             SEQUENCE OF 426-768 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
novel gene family.";
Cell 85:829-839(1996).
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Best Local Similarity
Matches 4; Conserv
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                                                               TISSUE-Brain;
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Search completed: November 1, 2002, 14:47:46 Job time: 2.36013 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 1, 2002, 14:43:58; Search time 0.742765 Seconds Run on:

(without alignments) 905.569 Million cell updates/sec

US-09-606-129A-18 41 1 KKRIMHC 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result No.	Score	Ouery Match	Length	DB	. di	Description
-	4.1	100.0	295	. 2	A42268	biliverdin reducta
7	41	100.0	633	~	T04537	hypothetical prote
m	38	92.7		7	G02066	യ
4	38	92.7		7	S62624	biliverdin reducta
S	36	87.8	512	7	н86206	hypothetical prote
9	34	82.9	401	7	F85015	ß
7	34	ď	431	7	T01723	
80	33	Ö	189	~	A38117	hypothetical prote
6	33	o.		~	AD2414	ø
10	33			~	AE2064	transposase all206
11	33	ö		N	AF2052	transposase all197
12	33	80.5		~	AF2152	
13	33			~	AG1875	transposase alr055
14	33			~	AG2037	transposase alr185
15	33	80.5		~	T02486	hypothetical prote
16	33	80.5		~	S50490	_
17	32	78.0		~	B64845	
18	32	78.0			A99791	hypothetical prote
	32	78.0	1.07		D85651	
20	32	78.0			149668	binding protein -
21	32	78.0			JC1365	FK506/rapamycin-bi
22	32	78.0			B65086	hydrogenase (EC 1.
23	32	78.0			A91114	hydrogenase-2 smal
24	32				A85959	hydrogenase-2 smal
25	32				AE0885	hydrogenase-2 smal
56	32		37	~	A82213	methylcitrate synt
27	32		497	~	C86463	hypothetical prote
28		78.0	51	~	T23827	
29	32	78.0	521	~	C88827	protein M7.2 (impo

2 T07047 leucyl 1 2 T070849 leucyl 1 S41376 leucyl 1 2 A10092 leucyl 1 2 A10092 leucyl 1 2 T070940 leucyl 2 T45004 leucyl 2 T46004 leucyl 2 T45004 leucyl 2 T32784 leucyl 2 T48373 leucyl 2 T4	.,.		78.0	266	7	T07850	
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31 75.6 106 1 R6UTGA ribosomal pro 13 75.6 1106 1 R6UTGA hypothetical			75.6	100	7	AI0092	probable membrane
31 75.6 137 2 746904 hypothetical 13 75.6 144 2 144100 C6 protein - 15.6 15.2 73784 hypothetical 13 75.6 279 2 710361 hypothetical 13 75.6 321 2 748373 hypothetical 13 75.6 383 2 551651 cyclin delta-13 75.6 476 2 717330 hypothetical 15.6 504 2 JC4775 hypothetical 15.6 504 2 JC4775 hypothetical 16.5 504 2 JC4775 hypothetical 17.5 6 504 2 JC4775 hypothetical 17.5		_	75.6	106		R6UT6A	ribosomal protein
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31 75.6 451 1 F64155 hypothetical. 31 75.6 476 2 T17330 hypothetical. 31 75.6 504 2 JC4775 interferon-in. ALIGNMENTS		_	ω,	383	7	S51651	cvclin delta-2 - A
31 75.6 476 2 T17330 hypothetical 31 75.6 504 2 JC4775 interferon-in ALIGNMENTS		_	'n	451	1	F64155	hypothetical prote
6 504 2 JC4775 ALIGNMENTS	44 3.	_	75.6	476	~	T17330	
ALIGNMENTS	45 3.	7	75.6	504	0	JC4775	interferon-induced
						ALIGNMENTS	
	A42268						
2.268	liverdin re	duct	ase (E	2 1.3.	1.2	) - rat	
2268 1iverdin reductase (EC 1.3.1.24) - rat	Species: Rat	ttus	norve	gicus	S S	way rat)	
A42268 biliverdin reductase (EC 1.3.1.24) - rat C;Species: Rattus norvegicus (Norway rat)	Date: 04-Man	r-19	93 #se	dneuce	ir Fe	ision 18-Nov-1994 #tex	xt_change 05-Nov-1999
A42268 bbliverdin reductase (EC 1.3.1.24) - rat C;Species: Rattus norvegicus (Norway rat) C;Dete: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999	O J C C F K . WO T D D D D C C F K . D	477					

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A:Till: Expression and characterization of a cDNA for rat kidney biliverdin reductas A:Till: Expression and characterization of a cDNA for rat kidney biliverdin reductas A:Reference number: A42268; MUID:92156147
A:Recession: A42268
A:Status: preliminary: not compared with conceptual translation A:Residues: preliminary: not compared with conceptual translation A:Residues: 1-295 A:FAK>
A:Cross-references: GB:M81681; NID:9203177; PIDN:AAA40830.1; PID:9203178
A:Ross-references: kidney
A:Note: Sequence extracted from NCBI backbone (NCBIP:82800)
C:Keywords: liver; oxidoreductase
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O
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R; Fakhrai, H.; Maines, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111111
274 KKRIMHC 280
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hypothetical protein F28J12.70 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999
C.Accession: T04537
R.Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro submitted to the Protein Sequence Database, February 1998
A.Reference number: 215377
A.Accession: T04537
A.Molecule type: DNA
A.References: EMBL:AL021710
A.Eross-references: EMBL:AL021710
A.Experimental source: cultivar Columbia; BAC clone F28J12

A; Map position: 4 A; Introns: 281/3; 303/3; 442/1; 614/3 A; Note: F28J12.70

Caps ö Query Match 100.0%; Score 41; DB 2; Length 633; Best Local Similarity 100.0%; Pred. No. 0.95; Matches 7; Conservative 0; Mismatches 0; Indels

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1 KKRIMHC 7

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qq

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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86206
B:Theologis, A.: BECKer, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.: White, O.; Alon Chin, C.W.; Chung, M.K.; Coon, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
AAuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
AAuthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
A.Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-phosphatidylinositol-4-phosphate 5-kinase type II homolog - Arabidopsis thaliana N;Alternate names: protein A_IG002N01.9 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999 C;Accession: T01723 R;Scheet, P.; Maggi, L. submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:NC_001268; NID:97267616; PIDN:CAB80928.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE005172; NID: 98954028; PIDN: AAF82202.1; GSPDB: GN00141
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18;
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A; Reference number: 214407
A; Accession: T01723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 8
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Pred. No. 1
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A;Molecule type: DNA
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71.4%;
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85.7%;
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-512 <STO>
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236 KKRLLHC 242
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C; Species: Homo sapiens (man)
C; Date: 28-oct-1996 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
C; Accession: 865624; 862622; 829736
R; Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
R*Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
A; Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
A; Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization
A; Reference number: 862622; MUID:96202961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 3-24, X', 26-27, X', 29-36,48-74;228-234;235-248 <MAW>
A;Note: the sequence of peptide 1 from page 323 seems not to belong to this protein
C;Genetics:
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A;Accession: S62622
                                                                                                                                                                  biliverdin reductase (EC 1.3.1.24) - human
N.Alternate names: blilverdin IX-alpha reductase
C.Species: Homo sapiens (man)
C.Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
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A; Molecule type: protein
A; Residues: 3-24, 'x', 26-27, 'x', 29-36; 48-74; 228-234; 235-248 < MAF>
R; Maines, M.D.; Trakshel, G.M.
Ardine: Biochem. Biophys. 300, 320-326, 1993
A; Title: Purification and characterization of human biliverdin reductase.
A; Reference number: S29736; MUID:93143333
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C;Keywords: oxidoreductase
F;3-296/Product: billverdin reductase IX-alpha #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 296;
                                                                                                                                                                                                                                                                C. Accession: G02066
R. Komuro, A.; Tobe, T.; Nakano, Y.; Yamaguchi, T.; Tomita, M. submitted to the EMBL Data Library, August 1995
A. Reference number: H00768
A. Accession: G02066
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Rolecule type: mRNA
A. Residues: 1-296 < KOMN
A. Residues: 1-296 < KOMN
A. Cross-references: EMBL: U34877; NID: 91143231; PID: 91143232
C. Keywords: oxidoreductase
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bypothetical protein [imported] - Arabidopsis thaliana
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Pred. No. 2;
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biliverdin reductase (EC 1.3.1.24) - human
N;Alternate names: biliverdin IX-alpha reductase
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Pred. No. 2;
1; Mismatches
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85.7%; Pred. No. 3
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85.7%;
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Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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A; Residues: 1-296 <MAI>
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591 KKRIMHC 597
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275 KKRILHC 281
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275 KKRILHC 281
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposase alr2773 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change ll-Jan-2002
C;Accession: AF2152
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamotc, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213; 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
                                                                                                                                                                                                                                                                                C.Accession: AE2064
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res, 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A.Recession: AE2064
A.Recession: AE2064
A.Status: preliminary
A.Molecule type: DNA
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                                                                                                                                                                          C:Species: Anabaena sp. A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
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A;Molecule type: DNA
A;Residues: 1-189 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73671.1; PID:g17131062; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-189 <KUR>
A;Residues: 1-189 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73766.1; PID:g17131158; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                           transposase all2067 [imported] - Anabaena sp. (strain PCC 7120)
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Pred. No. 15;
1; Mismatches
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Pred. No. 15;
1; Mismatches
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71.4%;
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llarity 71.4%;
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Matches 5; Conserv
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|||| KKRLKHC 177
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Cispecies: Anabaena sp.
Cispecies: Anabaena sp.
Cispecies: Anabaena sp.
Cispecies: 24-0ul-1992 #sequence_revision 24-Jul-1992 #text_change 15-Oct-1999
Cispecies: A38117
R.Alam, J.: Vrba, J.M.; Cai, Y.: Martin, J.A.; Weislo, L.J.; Curtis, S.E.
J. Bacteriol. 173, 5778-5783, 1991
A.Title: Characterization of the IS895 family of insertion sequences from the cyanobacte A:Reference number: A38117
A.Accession: A38117
A.Accession: A38117
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-189 <ALA>
A.Residues: 1-189 <ALA>
A.Residues: 1-189 <ALA>
A.Residues: 1-180 <ALA
A.Residues
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A; Residues: 1-189 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76567.1; PID:g17134005; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
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A;Introns: 40/2; 94/3; 161/3; 224/2; 255/1; 271/1; 303/1; 339/2
A;Note: A_IG002N01.9
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A;Residues: 1-431 <SCH>
A;Cross-references: EMBL:AF007269; NID:92191126; PID:92191143
A;Experimental source: cultivar Columbia
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Pred. No. 15;
1; Mismatches
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Pred. No. 19;
0; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Similarity 85.7%;
6; Conservative
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A; Status: preliminary
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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K; Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E DNA Res. 8, 205-213, 2001
NA Res. 9, 205-213, 2001
NA, Title. Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
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                                                                 A; Molecule type: DNA
A; Residues: 1-189 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74472.1; PID:g17131866; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: a1r2773
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A;Experimental source: strain PCC 7120
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A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2152
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5, Conservative
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A;Molecule type: DNA
A;Residués: 1-189 <KUR>
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                                                Status: preliminary
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171 KKRLKHC 177
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A; Molecule type: DNA
A; Residues: 1.508 «ROUS
A; Cross-references: EMBL:AC004680; NID:93420043; PID:93420052
A; Experimental source: cultivar Columbia
R; Lin, X; Kaul, S;; Stousley, S.D; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                               S.M.; K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: B84703
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                                                                                                                                                                               hypothetical protein At2g29990 [imported] - Arabidopsis thaliana N;Alernate names: hypothetical protein F23F19
N;Alternate names: hypothetical protein F23F19
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02486; B84703
R;Rounsley, S.D; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence. A;Recession: T02486
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE002093; NID: q3420052; PIDN: AAC31853.1; GSPDB: GN00139
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C;Superfamily: NADH dehydrogenase
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Pred. No. 36;
3; Mismatches
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Residues: 1-508 <STO>
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| 171 KKRLKHC 177
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